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161646

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From: Hamud, Fozia
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Subject: sequence search 10/717,282

Please search 10/717,282, SEQ ID NO: 2 full length and residues 36-753; SEQ ID NO:1 full length and 86-234 against commercial data bases. thanks

Fozia Hamud
Patent Examiner
Remsen 4D64
Mail Box: Remsen 4C70
(571) 272-0884
Art Unit 1647

STIC-Biotech/ChemLib
10/717,282
10/717,282

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Searcher: _____
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Date Searcher Picked up: _____
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Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
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Other(Specify): _____

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| Result No. | Score | Query | | Length | DB | ID | Description |
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| | | Match | % | | | | |
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| 3 | 2289 | 96.1 | 2341 | 6 | AX364576 | Sequence | AX364576 Sequence |
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| 6 | 2215.4 | 93.0 | 3083 | 6 | AX251723 | Sequence | AX251723 Sequence |
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| 1921 | Qy | GAGTGACTTCTGCTTAAAGGTAGAGCGGCTGTTTCTTGGGGCAACCGGACCGATC | 1980 |
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| 1981 | Qy | CCAGCACAGAGTCAAGTATGGGGCTGAGCAAGAGCGGGAGGCGCGGCTGCCCTTGA | 2040 |
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| 2281 | Qy | GTCAATGCAAGCAGATCTGTTGTCGCGAGCTACACTGATGAACCTCAACGCGGTGCGCCC | 2340 |

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| Db | 2281 | GTCAATGCAAAAGCAGAAUCTTGGTTGCCGCACTACTGATGAACACTCAACGCGGCCCGCCCC | 2344 |
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| AX364576 | | | |
| LOCUS | AX364576 | 2341 bp | linear |
| DEFINITION | Sequence 7 from Patent WO0208259. | | PAT 15-FEB-2002 |
| ACCESSION | AX364576 | | |
| VERSION | AX364576.1 | GI:18696536 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | Presnell,S.R., Kuestner,R.E. and Gao,Z. | | |
| TITLE | Human cytokine receptor | | |
| JOURNAL | Patent: WO 0208259-A 7 31-JAN-2002; | | |
| | ZymoGenetics, Inc. (US) | | |
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| Best Local Similarity | 98.2%; | Pred. No. 0; | |
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RESULT 4
AF494208
LOCUS
DEFINITION
ACCESSION

4477 bp mRNA linear PRI 08-DEC-2003
Homo sapiens interleukin 17 receptor-like protein long form
(IL17RLM) mRNA, complete cds; alternatively spliced.
AF494208

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| VERSION | AF494208.1 | GI:21667503 | |
| KEYWORDS | Homo sapiens (human) | | |
| SOURCE | Homo sapiens | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 4477) | | |
| AUTHORS | Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L., and Chang, Z. | | |
| TITLE | hSef inhibits PC-12 Cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling | | |
| JOURNAL | J. Biol. Chem. 278 (50), 50273-50282 (2003) | | |
| PUBMED | 12958313 | | |
| REFERENCE | 2 (bases 1 to 4477) | | |
| AUTHORS | Xiong, S.Q., Huang, G.R., Zhao, Q.H., Chen, P.L., Rong, Z.L., Ye, X.Y., Chen, Y., Liu, L., Fu, X.Y. and Chang, Z.J. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (22-MAR-2002) Tsinghua Institute of Genome Research, Department of Biological Sciences and Biotechnology, and School of Medicine, Tsinghua University, Beijing 100084, P.R. China | | |
| FEATURES | Location/Qualifiers | | |
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| Query Match | 95.8%; Score 2282.6; DB 9; Length 4477; | | |
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DEFINITION Sequence 13 from Patent WO0190358.
ACCESSION AX350979
VERSION AX350979.1 GI:18616355
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Gorman, D.M.
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JOURNAL Patent: WO 0190358-A 13 29-NOV-2001;
SCHERING CORPORATION (US)
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AX251723
LOCUS AX251723 3083 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 1 from Patent WO0168859.
ACCESSION AX251723
VERSION AX251723.1 GI:15985081
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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| AUTHORS | Jing.S. | |
| TITLE | IL-17 receptor like molecules and uses thereof | |
| JOURNAL | Patent: WO 0168959-A 1 20-SEP-2001; | |
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RESULT 8
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DEFINITION Sequence 15 from Patent WO0214358.
ACCESSION AX392973
VERSION AX392973.1 GI:19701020
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Edmonds,B.T., Micanovic,R., Ou,W., Su,E.W., Tschang,S.H. and Wang,H.
TITLE Novel secreted proteins and their uses
JOURNAL Patent: WO 0214358-A 15 21-FEB-2002; ELI LILLY AND COMPANY (US)
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VERSION AK093074.1 GI:21751823
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ORGANISM Homo sapiens
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Nagai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
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Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R.,
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Isogai, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 2894)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazuo-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel.81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
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construction: Helix Research Institute (HRI) (supported by Japan
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| AUTHORS | Xiong,S., Zhao,Q., Rong,Z., Huang,G., Huang,Y., Chen,P., Zhang,S., Liu,L. and Chang,Z. |
| TITLE | hSef Inhibits PC-12 Cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling |
| JOURNAL | J. Biol. Chem. 278 (50), 50273-50282 (2003) |
| PUBMED | 12958313 |
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| TITLE | Direct Submission |
| JOURNAL | Submitted (22-VAR-2002) Tsinghua Institute of Genome Research, Department of Biological Sciences and Biotechnology, and School of Medicine, Tsinghua University, Beijing 100084, P.R. China |
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| AUTHORS Wiemann, S. | | | |
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| JOURNAL Patent: WO 0112659-A 616 22-FEB-2001; | | | |
| German Human Genome Project (DE) | | | |
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Db 938 CATACATGCAGCACTCCCAAGAGAGAGGGCTCCGGCCGGCCGGAAGGCTTTCTCTGCT 997

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RESULT 13

LSM805220 2406 bp mRNA linear PRI 12-JUL-2002

LOCUS Homo sapiens mRNA; cDNA DKFp434L0320 (from clone DKFp434L0320).

DEFINITION AL833913

ACCESSION AL833913.1 GI:21739453

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2406)

AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2002) GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuherberg, Germany

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing Consortium of the German Genome Project. This clone (DKFp434L0320) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.

FEATURES

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| Db | 578 | CGCAAACTTCGGCTTCGGTTCTTCTATCTTCACTAAGCTCAAGCAAGCAAGACCTT | 637 |
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| Db | 758 | TGATGATTTATGCTTTAAAGCAGTGCACTCCCGTGGCGCGGCCCATCAGAGCGGTGG | 817 |
| Qy | 1032 | CCATCAGTGCATCTGGTGTAGTCATATCGGCATTCGCGAGCTCTTCACTGTGATGTGC | 1091 |
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| Db | 878 | GCAAGAGCAACAAGAAATATATATTCAATTTAGATGAAGAGCTCTGAGTCTTTCCA | 937 |
| Qy | 1152 | CATACATCAGCATCTCCCAAGAGAGAGGCTCGGCGCGCGCGGAGGCTTTCTGTGCT | 1211 |
| Db | 938 | CATACATCAGCATCTCCCAAGAGAGGCTCGGCGCGCGCGGAGGCTTTCTGTGCT | 997 |
| Qy | 1212 | ATTCAGTAAAGATGCGCAGAAATCAATGAATGCTGTCAGTGTTCGCTTACTTCTCC | 1271 |
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| Qy | 1392 | GTTCCAAAGGTATGAAGTACTTTGTGGAAGAAGAACTACAAACAAAGAGAGTGGCC | 1451 |
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| Qy | 2112 | CAGGCATCTATGACTCTGTGCTGCTCATCCAGCTGTCTGCTGCTGCTGCTGCTGCTG | 2171 |
| Db | 1898 | CAGGCATCTATGACTCTGTGCTGCTCATCCAGCTGTCTGCTGCTGCTGCTGCTGCTG | 1957 |
| Qy | 2172 | TCTCGACGGAACAGACAGAAAGCTTCCCTGACGAGAGCGTGTCTTCTTCCAGGCC | 2231 |
| Db | 1958 | TCTCGACGGAACAGACAGAAAGCTTCCCTGACGAGAGCGTGTCTTCTTCCAGGCC | 2017 |
| Qy | 2232 | TGGGTGAGGAGAACTCTCTGCTGCTTCTTCCAGCTCTCTCTCTCTCTCTCTCTCTCT | 2291 |
| Db | 2018 | TGGGTGAGGAGAACTCTCTGCTGCTTCTTCCAGCTCTCTCTCTCTCTCTCTCTCTCT | 2077 |
| Qy | 2292 | CAGATCTTGGTTCGCGCAGCTACACTGATGAATCTCAACGCGTGCCTCTTGTAAACAA | 2351 |
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| Qy | 2352 | ACGAAAGAGTCTAAGCATTTGCCACTTTAGCTG | 2383 |
| Db | 2138 | ACGAAAGAGTCTAAGCATTTGCCACTTTAGCTG | 2169 |

| | | | | |
|------------|---|-------------|--------|-----------------|
| RESULT 14 | BC038369 | 4490 bp | linear | PRI 24-JUN-2004 |
| LOCUS | BC038369 | 4490 bp | mRNA | |
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| ACCESSION | BC038369.1 | GI:23512250 | | |
| KEYWORDS | Homo sapiens (human) | | | |
| SOURCE | Homo sapiens | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| REFERENCE | 1 (bases 1 to 4490) | | | |
| AUTHORS | Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Frange,C., Raha,S.S., Loquelliano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kerteman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,W.I., Skalski,U., Smalusi,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A. | | | |
| TITLE | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences | | | |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) | | | |
| PUBMED | 12477932 | | | |
| REFERENCE | 2 (bases 1 to 4490) | | | |
| AUTHORS | Strausberg,R. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (01-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | | | |
| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov | | | |
| COMMENT | Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: ang@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A. | | | |
| FEATURES | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 72 Row: h Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24308146. Location/Qualifiers 1. .4490 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4830807" /tissue_type="Testis" /clone_lib="NIH MGC 97" | | | |

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RESULT 15
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spliced.
ACCESSION AY489047
VERSION AY489047.1 GI:42411054
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2364)
AUTHORS Preger,B., Ziv,I., Shabtay,A., Sher,I., Tsang,M., Dawid,I.B.,
Altuvia,Y. and Ron,D.
TITLE Alternative splicing generates an isoform of the human SeF gene
with altered subcellular localization and specificity
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101 (5), 1229-1234 (2004)
PUBMED 14742870
REFERENCE 2 (bases 1 to 2364)
AUTHORS Ron,D.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2003) Biology, Technion, Israel Institute of
Technology, Haifa 32000, Israel
FEATURES
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location/Qualifiers
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ORIGIN

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Qy 268 CAGCAGAAACAGTGGGCTGTACAACATCACCTTCAATATGACAAATGTGACCACTTCT 327
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| Qy | 1828 | CCATCTCTCTCCACTGCGCTACCGGGAGCCAGTCTTTCGAGAAAATTTGATTCGGGCTTTGGT | 1887 | |
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| Db | 1876 | TTTAAATGATGTCTATGTGCAAAACGAGGCTCGAGAGTGAATTTCTGCTTAAAGGTAGAGGC | 1935 | |
| Qy | 1948 | GGCTGTTCTTTGGGCAACCGGACCCAGCTCCACGACGAGAGTCAGCATGGGGGCT | 2007 | |
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| Qy | 2068 | GCAACGCGTGAAGCCGGAGCCCTCGGACATGCCCGGGACTCAGGCAATCTATGACTC | 2127 | |
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| Qy | 2188 | AGAAACGCTTCTCCCTGACGAGAGCGTGTCTCTCTTTCAGGCGCTGGGTGAGGAGGAACC | 2247 | |
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us-10-717-282-1.rge

Sat Aug 13 10:40:49 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2005, 19:37:18 ; Search time 1348.1 Seconds
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 5 | 2215.4 | 93.0 | 3083 | 4 | AAS15346 DNA encod |
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| 32 | 71.4 | 3.0 | 3120 | 10 | ADD25545 Binding d |
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| 43 | 71.4 | 3.0 | 3223 | 4 | AAf57188 Human IL- |
| 44 | 71.4 | 3.0 | 3223 | 4 | AAO2815 Human int |
| 45 | 71.4 | 3.0 | 3223 | 12 | ADJ88264 Human IL- |

ALIGNMENTS

RESULT 1
ABA95031
ID ABA95031 standard; DNA; 2383 BP.

AC ABA95031;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 nucleotide sequence.

XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 86..2347

FT FT /*tag= a

FT FT /product= "Zcytor18"

PN WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX P-PSDB; ABB07626.

XX New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
PS Claim 5; Page 85-90; 119pp; English.
XX The invention relates to an isolated cytokine receptor polypeptide
CC

CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 nucleotide sequence
XX

SQ Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;

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| Qy | AGGAGTGGCGCGGCTCGGGAAAGGAGAGCTCTTCTGTGTGGCTGTGAGCAGCTTCG 1500 |
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| Db | CCAGAGCGGGGCGAGCACACCGCAGAGGGCAGCAGAGGAACTACTTTCCGGAGCAAGTC 1740 |
| Qy | AGGCGGTCCTTATGCTGCGCATTTGCAACATGCAACAGTTTATGACGAGGAGCCGGA 1800 |
| Db | AGGCGGTCCTTATGCTGCGCATTTGCAACATGCAACAGTTTATGACGAGGAGCCGGA 1800 |
| Qy | CTGCTTCGAAAGCAGTTCGTTCCCTTCCATCTCCCTCACTGCGCTACCCGGAGCCAGT 1860 |
| Db | CTGCTTCGAAAGCAGTTCGTTCCCTTCCATCTCCCTCACTGCGCTACCCGGAGCCAGT 1860 |
| Qy | CTTGAGAAAATTTGATTCGGGCTTGGTTTAAATGATGTCTATGTGCAACACAGGCGCTGA 1920 |
| Db | CTTGAGAAAATTTGATTCGGGCTTGGTTTAAATGATGTCTATGTGCAACACAGGCGCTGA 1920 |

QY 721 CTTCTGGAAGCTCGGAACCTGAAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTT 780
DB 721 CTTCTGGAAGCTCGGAACCTGAAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTT 780
QY 781 CGACCATCAGCCGCAAACTTTCGGCTTCGGTTTCTTCTATCTTCACTAACAAGCTCAAGCA 840
DB 781 CGACCAGCAACCGCAAACTTTCGGCTTCGGTTTCTTCTATCTTCACTAACAAGCTCAAGCA 840
QY 841 CGAAGGACCTTCAAGCGAAGACCTGTGAAGCAGGAGCAAACTACAGAGACGACCAAGTG 900
DB 841 CGAAGGACCTTCAAGCGAAGACCTGTGAAGCAGGAGCAAACTACAGAGATGACCAAGCTG 900
QY 901 CCTCTTCAAAATGTTTCTCAGGGGATTAATAATTGAGCTGGTGGATGACACTTAACAC 960
DB 901 CCTCTTCAAAATGTTTCTCAGGGGATTAATAATTGAGCTGGTGGATGACACTTAACAC 960
QY 961 AACAGAAAAGTGATGCAATTATGCTTTAAAGCCAGTGCACTCCCGTGGGCGGGCCCAT 1020
DB 961 AACAGAAAAGTGATGCAATTATGCTTTAAAGCCAGTGCACTCCCGTGGGCGGGCCCAT 1020
QY 1021 CAGAGCCGTGGCCATCAGAGTGCCACTGGTAGTCATATCGGCATTCGGAGCGCTTTCAC 1080
DB 1021 CAGAGCCGTGGCCATCAGAGTGCCACTGGTAGTCATATCGGCATTCGGAGCGCTTTCAC 1080
QY 1081 TGTGATGTGCGCAAGAGCAACAAAGAAAATATATATTCACATTTAGATGAAGAGAGCTC 1140
DB 1081 TGTGATGTGCGCAAGAGCAACAAAGAAAATATATATTCACATTTAGATGAAGAGAGCTC 1140
QY 1141 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGGCGCAAGGT 1200
DB 1141 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGGCGCAAGGT 1200
QY 1201 CTTTCTCTGCTATTCAGTAAAGATGGCCAGAAATCAGATGAATGCTGCCAGTGTTCGC 1260
DB 1201 CTTTCTCTGCTATTCAGTAAAGATGGCCAGAAATCAGATGAATGCTGCCAGTGTTCGC 1260
QY 1261 CTACTTCTCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAG 1320
DB 1261 CTACTTCTCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAG 1320
QY 1321 CCTCTGTAGAGAGGCGCAGAGAGATGGTTCATCCAGAAAGATCCACGAGTCCCAGTTTCA 1380
DB 1321 CCTCTGTAGAGAGGCGCAGAGAGATGGTTCATCCAGAAAGATCCACGAGTCCCAGTTTCA 1380
QY 1381 CATGTGTGTTTTCACAAAGGTATGAAGTACTTGTGACAGAGAGAACTACAAACACAA 1440
DB 1381 CATGTGTGTTTTCACAAAGGTATGAAGTACTTGTGACAGAGAGAACTACAAACACAA 1440
QY 1441 AGGAGTGGCGAGGCTCGGGAAAGAGAGCTTCTCTGTGGCGGTGTGAGCCATTGC 1500
DB 1441 AGGAGTGGCGAGGCTCGGGAAAGAGAGCTTCTCTGTGGCGGTGTGAGCCATTGC 1500
QY 1501 CGAAAAGCTCCGCCAGGCGCAAGCAGAGTTCTGTCGCGCGCTCAGCAAGTTTATCGCGGT 1560
DB 1501 CGAAAAGCTCCGCCAGGCGCAAGCAGAGTTCTGTCGCGCGCTCAGCAAGTTTATCGCGGT 1560
QY 1561 CTACTTTGATTATTCCTCGAGGAGAGAGCTCCCGGTATCTAGACCTGAGTACCAAGTA 1620
DB 1561 CTACTTTGATTATTCCTCGAGGAGAGAGCTCCCGGTATCTAGACCTGAGTACCAAGTA 1620
QY 1621 CAGACTCATGACATCTTCTCAGCTCTGTTCCACTTGCACCTCCGAGACCGGCT 1680
DB 1621 CAGACTCATGACATCTTCTCAGCTCTGTTCCACTTGCACCTCCGAGACCGGCT 1680
QY 1681 CCAGGAGCGGGGCGACACCGCAGAGGCGAGCAAGAGAACTACTTCCGAGCAAGTC 1740
DB 1681 CCAGGAGCGGGGCGACACCGCAGAGGCGAGCAAGAGAACTACTTCCGAGCAAGTC 1740
QY 1741 AGGCGGTCTCTATAGTCGCCATTTGCAACATGCAACAGTTTATGACGAGGAGCCGA 1800
DB 1741 AGGCGGTCTCTATAGTCGCCATTTGCAACATGCAACAGTTTATGACGAGGAGCCGA 1800
QY 1801 CTGGTTTCAAAAAGCAGTTTCGTTCCCTTCCATCTCCTCCTCAGCTGCGCTACCGGAGCCAGT 1860

DB 1801 CTGGTTTCAAAAAGCAGTTTCGTTCCCTTCCATCTCCTCCACTGCGCTACCGGAGCCAGT 1860
QY 1861 CTTGGAGAAATTTGATTTGGGCTTGGTTTAAATGATGTCATGTGCAAAACAGAGGCTGA 1920
DB 1861 CTTGGAGAAATTTGATTTGGGCTTGGTTTAAATGATGTCATGTGCAAAACAGAGGCTGA 1920
QY 1921 GAGTGACTTCTGCTAAAGGTAGAGGCGCTGTTTGGGGCAACCGGACCCAGCCGACTC 1980
DB 1921 GAGTGACTTCTGCTAAAGGTAGAGGCGCTGTTTGGGGCAACCGGACCCAGCCGACTC 1980
QY 1981 CCAGCAGAGAGTCAGCATGGGGCTTGGACCAAGACGGGAGGCGCCGCTGCGGACT 2040
DB 1981 CCAGCAGAGAGTCAGCATGGGGCTTGGACCAAGACGGGAGGCGCCGCTGCGGACT 2040
QY 2041 CGGTAGGCGCGCTTCCAAACCTTGTCTGTCACACAGGTGAAGCGGCGCCCTCGGACAT 2100
DB 2041 CGGTAGGCGCGCTTCCAAACCTTGTCTGTCACACAGGTGAAGCGGCGCCCTCGGACAT 2100
QY 2101 GCCGCGGACTCAGGCACTATGACTGCTGTGCTGCCCTCATCCGAGCTGTCTTGCCACT 2160
DB 2101 GCCGCGGACTCAGGCACTATGACTGCTGTGCTGCCCTCATCCGAGCTGTCTTGCCACT 2160
QY 2161 GATGGAAGGACTCTCGACGGACCAAGACAGAAACGTCTTCCTTGAACGAGAGCGTGTCTC 2220
DB 2161 GATGGAAGGACTCTCGACGGACCAAGACAGAAACGTCTTCCTTGAACGAGAGCGTGTCTC 2220
QY 2221 CTCTTACGGCTGGGTGAGGAGGAACCTCTGCGCCCTTCTTCCAAAGCTCTCTTCTGG 2280
DB 2221 CTCTTACGGCTGGGTGAGGAGGAACCTCTGCGCCCTTCTTCCAAAGCTCTCTTCTGG 2280
QY 2281 GTCATGCAAAAGCAGATCTTGTGTCGCGCAGTACACTGATGAACCTCCACGCGGTCGCC 2340
DB 2281 GTCATGCAAAAGCAGATCTTGTGTCGCGCAGTACACTGATGAACCTCCACGCGGTCGCC 2340
QY 2341 TTTGTAAACAAAACGAAAGAGCTTAAGCAITTGCCAATTAGCTG 2383
DB 2341 TTTGTAAACAAAACGAAAGAGCTTAAGCAITTGCCAATTAGCTG 2383

RESULT 3
ABA95035
ID ABA95035 standard; DNA; 2341 BP.
XX ABA95035;
AC ABA95035;
DT 20-MAY-2002 (first entry)
XX Human cytokine receptor, Zcytor18 splice variant nucleotide sequence.
XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
XX erythroleukemia; chromosome 3p14.3; gene therapy; splice variant; ds.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 86..2305
FT /*tag= a
FT /product= "Zcytor18 splice variant"
XX
XX WO200208259-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US023253.
XX
XX 26-JUL-2000; 2000US-0220747P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Kuestner RE, Gao Z;
XX

DR WPI; 2002-217048/27.
XX P-PSDB; ABB07628.
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
PS Claim 5; Page 102-106; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 splice variant nucleotide sequence
XX
SQ Sequence 2341 BP; 550 A; 668 C; 625 G; 498 T; 0 U; 0 Other;
Query Match 96.1%; Score 2289; DB 6; Length 2341;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2341; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
QY 1 CGCGCGCGCCACCGCCACCTCGGGGCTGGCCAGCGGGCGGGCGGGCGGCAGAGAAC 60
DB 1 CGCGCGCGCCACCGCCACCTCGGGGCTGGCCAGCGGGCGGGCGGGCGGCAGAGAAC 60
QY 61 GGCCTGGCTGGCGGAGCGGACGGCCATGGCCCCGGTGGCTGACGCTCTGCTCGCTTCTT 120
DB 61 GGCCTGGCTGGCGGAGCGGACGGCCATGGCCCCGGTGGCTGACGCTCTGCTCGCTTCTT 120
QY 121 TACGGTCAACGGCTCGCTCAACGGCTCGGAGCTGGCTGGCGGCTGGCGGCTGGCGGCG 180
DB 121 TACGGTCAACGGCTCGCTCAACGGCTCGGAGCTGGCTGGCGGCTGGCGGCTGGCGGCG 180
QY 181 CGCGCGGGCGCGGACACCTGTGGCTGGAGGATGAAGCGGCTGCCCGACCCCGGCTTTG 240
DB 181 CGCGCGGGCGCGGACACCTGTGGCTGGAG----- 210
QY 241 TGTGCTAATGAGGAGTGGGCGGACGAGAGAACAGTGGGCTGTACACATCACCTT 300
DB 211 -----GGGAGTGGGCGGACGAGAGAACAGTGGGCTGTACACATCACCTT 258
QY 301 CAATATGACAACTTACACCTTACTTGAATCCAGTGGGAGCATGTGATGCTGACGC 360
DB 259 CAATATGACAACTTGTACCCTTACTTGAATCCAGTGGGAGAGCATGTGATGCTGACGC 318
QY 361 CCAGAAATACCAATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCAACATTTCTTTG 420
DB 319 CCAGAAATACCAATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCAACATTTCTTTG 378
QY 421 GTCCCGAGGGCCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGAGAGGCT 480
DB 379 GTCCCGAGGGCCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGAGAGGCT 438
QY 481 GAAGTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB 439 GAAGTCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 498
QY 541 TAGCTTCAAAAGAACTGGAATCTCAACCTTTCTTGAATATGAATTTGAAACGGA 600
DB 499 TAGCTTCAAAAGAACTGGAATCTCAACCTTTCTTGAATATGAATTTGAAACGGA 558
QY 601 TTATTTTCGTAAGGTTGTCCTTTTCTTTTCCATTAATAAAGCAATTTACACCTTTT 660
DB 559 TTATTTTCGTAAGGTTGTCCTTTTCTTTTCCATTAATAAAGCAATTTACACCTTTT 618

QY 661 CTTCTTTAGAAACCCGAGCCTGTGACCTGTTGTTACAGCCGAGCAATCTAGCTTGTAAACC 720
DB 619 CTTCTTTAGAAACCCGAGCCTGTGACCTGTTGTTACAGCCGAGCAATCTAGCTTGTAAACC 678
QY 721 CTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATCAGGCTGCTT 780
DB 679 CTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATCAGGCTGCTT 738
QY 781 CGACATCGACCGGACAACTTCGGCTTCGTTTCTTCTATCTTCACTCAACAGCTCAAGCA 840
DB 739 CGACATCGACCGGACAACTTCGGCTTCGTTTCTTCTATCTTCACTCAACAGCTCAAGCA 798
QY 841 CGAAGGACCTTTTAAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACAGCTG 900
DB 799 CGAAGGACCTTTTAAAGCGAAAGACCTGTAAGCAGGAGCAAACTACAGAGACGACAGCTG 858
QY 901 CCTCTTCAAAATGTTTCTCAGGGGATATATAATTCAGCTGGTGGATGACACTAAAC 960
DB 859 CCTCTTCAAAATGTTTCTCAGGGGATATATAATTCAGCTGGTGGATGACACTAAAC 918
QY 961 AACAGAAAGTGTATGATTCCTTAAAGCCAGTGCACCTCCCGTGGCGGGCCCAT 1020
DB 919 AACAGAAAGTGTATGATTCCTTAAAGCCAGTGCACCTCCCGTGGCGGGCCCAT 978
QY 1021 CAGAGCCGTGGCCCATCACAGTGCCACTGTGTAGTCAATATCGGCATTCGCGAGCTCTTCA 1080
DB 979 CAGAGCCGTGGCCCATCACAGTGCCACTGTGTAGTCAATATCGGCATTCGCGAGCTCTTCA 1038
QY 1081 TGTGATGTGGCGGAGAAAGCAAAAGAAATATATATTTACATTTAGATGAAGAGCTC 1140
DB 1039 TGTGATGTGGCGGAGAAAGCAAAAGAAATATATATTTACATTTAGATGAAGAGCTC 1098
QY 1141 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGCTTCGGCGCGCGCGAAGT 1200
DB 1099 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGCTTCGGCGCGCGCGAAGT 1158
QY 1201 CTTTCTCTGTATTTCCAGTAAAGATGGCCAGAAATCACAATGATGTCTGCTGATTTGCT 1260
DB 1159 CTTTCTCTGTATTTCCAGTAAAGATGGCCAGAAATCACAATGATGTCTGCTGATTTGCT 1218
QY 1261 CTACTTCTCAGAGCTTCTGTGGCTGTGAGGTGCTCTGAGACCTGTGGGAGAGCTTCA 1320
DB 1219 CTACTTCTCAGAGCTTCTGTGGCTGTGAGGTGCTCTGAGACCTGTGGGAGAGCTTCA 1278
QY 1321 CCTCTGTAGAGAGGCGAGAGAGATGGGTCAATCCAGAGATCCACAGTCCAGTTCAT 1380
DB 1279 CCTCTGTAGAGAGGCGAGAGAGATGGGTCAATCCAGAGATCCACAGTCCAGTTCAT 1338
QY 1381 CATTTGTGTTTGTTCGAAAGGTATGAAGTACTTTTGTGGAAGAAGAACTACAAACACAA 1440
DB 1339 CATTTGTGTTTGTTCGAAAGGTATGAAGTACTTTTGTGGAAGAAGAACTACAAACACAA 1398
QY 1441 AGGAGTGGCGGAGCTCGGGGAGAGAGAGCTCTTCTGTTGGCGGTGTGAGCATTGC 1500
DB 1399 AGGAGTGGCGGAGCTCGGGGAGAGAGAGCTCTTCTGTTGGCGGTGTGAGCATTGC 1458
QY 1501 CGAAAGTCTCGGAGCGCAAGCAGAGTTCGTCGGCGGCTCAGCAAGTTTATCGCGT 1560
DB 1459 CGAAAGTCTCGGAGCGCAAGCAGAGTTCGTCGGCGGCTCAGCAAGTTTATCGCGT 1518
QY 1561 CTACTTTGATTTATCTCGGAGGAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTA 1620
DB 1519 CTA CTTTGTATTTCTCGGAGGAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTA 1578
QY 1621 CAGACTATGAGCAATCTTCTCAGCTCTGTTTCCACTGTGCACTCCCGAGACCAAGCT 1680
DB 1579 CAGACTATGAGCAATCTTCTCAGCTCTGTTTCCACTGTGCACTCCCGAGACCAAGCT 1638
QY 1681 CCAGAGCGGGGAGGACACCGGAGCGGAGAGAGAGTACTTCCCGAGCAAGTTC 1740
DB 1639 CCAGAGCGGGGAGGACACCGGAGCGGAGAGAGAGTACTTCCCGAGCAAGTTC 1698

QY 1741 AGCGCGTCCCTATACGTGCGCATTTGCAACATGCACCAAGTTTATGACGAGGAGCCGA 1800
DB |||||||
QY 1699 AGCGCGTCCCTATACGTGCGCATTTGCAACATGCACCAAGTTTATGACGAGGAGCCGA 1758
DB |||||||
QY 1801 CTGTTTGGAAAGCAGTTTCCTTCCATCTCTCTCCATCTGCGCTACCGGAGCCAGT 1860
DB |||||||
QY 1759 CTGTTTGGAAAGCAGTTTCCTTCCATCTCTCTCCATCTGCGCTACCGGAGCCAGT 1818
DB |||||||
QY 1861 CTGAGAGAAATTTGATTCGGGCTTGTTTAAATGATGTGATGCAACACCGGCTGA 1920
DB |||||||
QY 1819 CTGAGAGAAATTTGATTCGGGCTTGTTTAAATGATGTGATGCAACACCGGCTGA 1878
DB |||||||
QY 1921 GAGTGACTTCCTTAAAGGTAGAGGCGCTGTTCTTGGGCAACCGGACCGGACTC 1980
DB |||||||
QY 1879 GAGTGACTTCCTTAAAGGTAGAGGCGCTGTTCTTGGGCAACCGGACCGGACTC 1938
DB |||||||
QY 1981 CCAGCAGAGAGTCAGCATGCGGCTTGACCAAGAGCGGAGCGCGCTGCTGCA 2040
DB |||||||
QY 1939 CCAGCAGAGAGTCAGCATGCGGCTTGACCAAGAGCGGAGCGCGCTGCTGCA 1998
DB |||||||
QY 2041 CGGTAGCGCCCTGCAACCCCTGCTGCACACGGTGAAAGCGGACCGCCCTCGGACAT 2100
DB |||||||
QY 1999 CGGTAGCGCCCTGCAACCCCTGCTGCACACGGTGAAAGCGGACCGCCCTCGGACAT 2058
DB |||||||
QY 2101 GCCGCGGACTCAGCATCTATGACTGCTGTGCTGCTCATCCGAGCTGTCTTGCCTACT 2160
DB |||||||
QY 2059 GCCGCGGACTCAGCATCTATGACTGCTGTGCTGCTCATCCGAGCTGTCTTGCCTACT 2118
DB |||||||
QY 2161 GATGAAGGACTCTCGACGACCAAGAACAGTCTTCTCTGACGGAGAGCGTGTCTC 2220
DB |||||||
QY 2119 GATGAAGGACTCTCGACGACCAAGAACAGTCTTCTCTGACGGAGAGCGTGTCTC 2178
DB |||||||
QY 2221 CTCTTACGCGCTGGTGAGGAGGAACCTCTGCTGCTTCTTCTTCTTCTTCTTCTG 2280
DB |||||||
QY 2179 CTCTTACGCGCTGGTGAGGAGGAACCTCTGCTGCTTCTTCTTCTTCTTCTTCTG 2238
DB |||||||
QY 2281 GTCATGCAAGCAGATCTTTGTTGCGCAGCTACATGATGAATCTCCACGCGGTGCGCCC 2340
DB |||||||
QY 2239 GTCATGCAAGCAGATCTTTGTTGCGCAGCTACATGATGAATCTCCACGCGGTGCGCCC 2298
DB |||||||
QY 2341 TTTGTAAACAAACGAAAGAGTCTAAGCATTTGCCACTTTAGCTG 2383
DB |||||||
QY 2299 TTTGTAAACAAACGAAAGAGTCTAAGCATTTGCCACTTTAGCTG 2341
DB |||||||

RESULT 4
AAS18134
ID AAS18134 standard; cDNA; 2786 BP.
XX
AC AAS18134;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX cytokine receptor subunit 8 (DCRS8) cDNA.
XX
KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss;
KW gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 70..2286
FT /*tag= a
FT /product= "Human DCRS8"
XX
XX WO200190358-A2.
XX
XX 29-NOV-2001.
XX
XX 23-MAY-2001; 2001WO-US016767.
XX
XX 24-MAY-2000; 2000US-0206862P.
XX
XX

(SCHE) SCHERING CORP.
Gorman DM;
WPI; 2002-106198/14.
P-PSDB; AAU11355.
Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
useful for detecting antibodies generated in response to presence of
increased protein levels or immunological disorders.
Claim 16; Page 21-25; 148pp; English.
The invention relates to primate and rodent DNAX cytokine receptor
subunit (DCRS) polypeptides and the polynucleotides encoding them. The
receptors, or their portions may be useful as phosphate labelling enzymes
to label general or specific substrates. The subunits may also be
functional immunogens to elicit recognising antibodies, or antigens
capable of binding antibodies. A combination, e.g., including a DCRS can
be used as an immunogen for the production of antisera or antibodies
capable of distinguishing between other cytokine receptor family members.
A purified DCRS can also be used as a reagent to detect antibodies
generated in response to the presence of elevated levels of expression,
or immunological disorders which lead to antibody production to the
endogenous receptor. This sequence represents cDNA encoding the human
DCRS8 polypeptide
Sequence 2786 BP; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;
Query Match 93.1%; Score 2218.6; DB 6; Length 2786;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 20; Indels 45; Gaps 2;
QY 27 CTGCGCAGCGCGCGCGCGCGCGCGCGCGCAGAGACGGCTGGCTGGGCGAGCGCAGGCCA 86
DB |||||||
QY 11 CGGCGCAGCAGCGCGCGCGCGCGCGCGCGCGCAGAGACGGCTGGCTGGGCGAGCGCAGGCCA 70
DB |||||||
QY 87 TGGCCCCGTGGCTGCAGCTCTGCTCCGTCTTCTTACGGTCAACGCTCTGCTCAACGGCT 146
DB |||||||
QY 71 TGGCCCCGTGGCTGCAGCTCTGCTCCGTCTTCTTACGGTCAACGCTCTGCTCAACGGCT 130
DB |||||||
QY 147 CGCAGCTGGCTGTGGCGCTGGCGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGGCT 206
DB |||||||
QY 131 CGCAGCTGGCTGTGGCGCTGGCGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTAGCT 190
DB |||||||
QY 207 GGAGGATGAAGCGGCTGCGCGCGCGCGCGCGCGCTTGTGTCTAATGAGGAGTGGGCGCAG 266
DB |||||
QY 191 GGA-----NGGGAGTGGGCGCAG 208
DB |||||||
QY 267 CCAGCAGAAACAGTGGGCTGTACAAATCAGCTTCAAAATATGACAAATTTGTACCACTACT 326
DB |||||||
QY 209 CCAGCAGAAACAGTGGGCTGTACAAATCAGCTTCAAAATATGACAAATTTGTACCACTACT 268
DB |||||||
QY 327 TGAATCCAGTGGGGAAGCATGTGATCTGACGCCAGAAATATCACCATCAGCAGTATG 386
DB |||||||
QY 269 TGAATCCAGTGGGGAAGCATGTGATCTGACGCCAGAAATATCACCATCAGCAGTATG 328
DB |||||||
QY 387 CTTGCCATGACCAAGTGGCAGTCAACATCTTTTGGTCCCGAGGGGCGCTCGGCATCGAAT 446
DB |||||||
QY 329 CTTGCCATGACCAAGTGGCAGTCAACATCTTTTGGTCCCGAGGGGCGCTCGGCATCGAAT 388
DB |||||||
QY 447 TCCTGAAAGGATTTTCGGGTAACTCTGGAGGAGCTGAAAGTCCGAGGGAAGACAGTGCCTAAC 506
DB |||||||
QY 389 TCCTGAAAGGATTTTCGGGTAACTCTGGAGGAGCTGAAAGTCCGAGGGAAGACAGNGCCAAC 448
DB |||||||
QY 507 AACTGATTTCTAAAGGATCCGAAAGCAGCTCAACAGTAGCTTCAAAAGAACTCGAATGGAAAT 566
DB |||||||
QY 449 AACTGATTTCTAAAGGATCCGAAAGCAGNTCAACAGTAGCTTCAAAAGAACTCGAATGGAAAT 508
DB |||||||
QY 567 CTCAACCTTTCTGAATATGAAATTTGAAACGGGATTTTGGTAAAGGTTTCTCCTTTTC 626
DB |||||||
QY 509 CTCAACCTTTTCTGAATATGAAATTTGAAACGGGATTTTTCGTAAGG---TTGCTCTTTT 565
DB |||||||

```
QY 627 CTTTCATTAATAAAGCAATTAACACCCCTTTCTTTCTTTAGAACCCGAGCTGTGACC 686
DB 628 CTTTCATTAATAAAGCAATTAACACCCCTTTCTTTCTTTAGAACCCGAGCTGTGACC 625
QY 687 TGTGTTTACAGCCGACCAATCTAGCTTGTAAACCTTCTTGGAGCCTCGAAACCTGAACA 746
DB 688 TGTGTTTACAGCCGACCAATCTAGCTTGTAAACCTTCTTGGAGCCTCGAAACCTGAACA 685
QY 747 TCAGCCAGCTGCTCGACATGACAGGTGCTTTCGACCATGACCGCACAACTTCGGCT 806
DB 748 TCAGCCAGCTGCTCGACATGACAGGTGCTTTCGACCATGACCGCACAACTTCGGCT 745
QY 807 TCCGTTTCTTCTATCTTCACTAAGCTCAAGCAGCAAGAGACCTTTCAAGCGAAAGACCT 866
DB 808 TCCGTTTCTTCTATCTTCACTAAGCTCAAGCAGCAAGAGACCTTTCAAGCGAAAGACCT 805
QY 867 GTAAGCAGAGCAAACTACAGAGACGACGAGTGTCTTCTTCAAAATGTTTCTCAGGGG 926
DB 868 GTAAGCAGAGCAAACTACAGAGATGACGAGTGTCTTCTTCAAAATGTTTCTCAGGGG 865
QY 927 ATTATATATTCAGCTGTGGATGACACTTAACACCAAGAAAGTGTGATGATATGCT 986
DB 928 ATTATATATTCAGCTGTGGATGACACTTAACACCAAGAAAGTGTGATGATATGCT 925
QY 987 TAAAGCAGTGCACCTCCCGTGGCGGCCCATCAGAGCCGTGCCATCAGAGTCCAC 1046
DB 988 TAAAGCAGTGCACCTCCCGTGGCGGCCCATCAGAGCCGTGCCATCAGAGTCCAC 985
QY 1047 TGGTAGTCATATCGGCATTCGCGAGCTTCTTCACTGTGATGTGCGCAAGAACCAAG 1106
DB 1048 TGGTAGTCATATCGGCATTCGCGAGCTTCTTCACTGTGATGTGCGCAAGAACCAAG 1045
QY 1107 AAAATATATATTCAGTGTGATGAGAGAGCTCTGAGTCTTCCACATACACTGACGAC 1166
DB 1108 AAAATATATATTCAGTGTGATGAGAGAGCTCTGAGTCTTCCACATACACTGACGAC 1105
QY 1167 TCCCAAGAGAGAGCTCCGCGCGCGCGCAAGGTCTTCTGCTATTTCAGTAAAGATG 1226
DB 1168 TCCCAAGAGAGAGCTCCGCGCGCGCGCAAGGTCTTCTGCTATTTCAGTAAAGATG 1165
QY 1227 GCCAGATCACAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
DB 1228 GCCAGATCACAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
QY 1287 GTGAGGTGCTGTGACCTGTGGAGAGCTTACGCTCTGTAGAGAGGCGAGAGAT 1346
DB 1288 GTGAGGTGCTGTGACCTGTGGAGAGCTTACGCTCTGTAGAGAGGCGAGAGAT 1285
QY 1347 GGGTCATCCAGAGATCCAGAGTCCAGTTCATCTGTTGTTTCCAAAGGTATGA 1406
DB 1348 GGGTCATCCAGAGATCCAGAGTCCAGTTCATCTGTTGTTTCCAAAGGTATGA 1345
QY 1407 AGTACTTGTGACAAAGAACTACAAACACAAAGAGGTGCGCGAGCTCGGGGAAAG 1466
DB 1408 AGTACTTGTGACAAAGAACTACAAACACAAAGAGGTGCGCGAGCTCGGGGAAAG 1405
QY 1467 GAGAGCTTCTTGTGCGGTGTGACGATTCGCAATTCGCGAAAGCTCGCGCAAGCAGA 1526
DB 1468 GAGAGCTTCTTGTGCGGTGTGACGATTCGCAATTCGCGAAAGCTCGCGCAAGCAGA 1465
QY 1527 GTTCGTCGCGGGCTCAGCAAGTTTATCGCGTCTTCTGATTTCTTCTGCGGGGAG 1586
DB 1528 GTTCGTCGCGGGCTCAGCAAGTTTATCGCGTCTTCTGATTTCTTCTGCGGGGAG 1525
QY 1587 AGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGCAATCTTCTCTCAGC 1646
DB 1588 AGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGCAATCTTCTCTCAGC 1585
QY 1647 TCTGTTCCACTGTGACCTCCGAGACCAAGGCTTCAGAGCGCGGCGAGCAACGCGAC 1706
DB 1648 TCTGTTCCACTGTGACCTCCGAGACCAAGGCTTCAGAGCGCGGCGAGCAACGCGAC 1645
QY 1707 AGGGCAGCAGAGGAACTACTTCCGAGCAAGTCCAGCGGTCCCTATACGTGCGCATTT 1766
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DB 1646 AGGGCAGCAGAGGAACTACTTCCGAGCAAGTCCAGCGGTCCCTATACGTGCGCATTT 1705
QY 1767 GCAACATCCACAGTTTATTCACGAGAGCGCGACTGCTTGCAAAAGCAGTTCGTTCCT 1826
DB 1768 GCAACATCCACAGTTTATTCACGAGAGCGCGACTGCTTGCAAAAGCAGTTCGTTCCT 1765
QY 1827 TCCATCTCTCTCCACTGCGCTACCGGAGCGAGCTTTCGAGAAATTTGATTCGGGCTGG 1886
DB 1828 TCCATCTCTCTCCACTGCGCTACCGGAGCGAGCTTTCGAGAAATTTGATTCGGGCTGG 1825
QY 1887 TTTTAAATGATGATGTCGAAAACGAGGCTTACGAGTGTCTGCTTAAAGGTAGAGG 1946
DB 1888 TTTTAAATGATGATGTCGAAAACGAGGCTTACGAGTGTCTGCTTAAAGGTAGAGG 1885
QY 1947 CGGCTGTTCTTGGGGCAACCGGACCGAGCTCCACGACGAGAGTCCAGATTCGGGGCC 2006
DB 1948 CGGCTGTTCTTGGGGCAACCGGACCGAGCTCCACGACGAGAGTCCAGATTCGGGGCC 1945
QY 2007 TGGACCAAGAGCGGGAGCGCGGCTGCTTTCGAGTGTGCGCCCTTGCAACCCCTGC 2066
DB 2008 TGGACCAAGAGCGGGAGCGCGGCTGCTTTCGAGTGTGCGCCCTTGCAACCCCTGC 2005
QY 2067 TGCACACGTTGAAAGCGCGGACCGCTCGGACATGCGCGGGACTTCAGGCACTTATGCT 2126
DB 2068 TGCACACGTTGAAAGCGCGGACCGCTCGGACATGCGCGGGACTTCAGGCACTTATGCT 2065
QY 2127 CGTGTGCTCTCATCCGAGCTGTCTGCGCACTGATGGAAGGACTTCGACGACCCAGA 2186
DB 2128 CGTGTGCTCTCATCCGAGCTGTCTGCGCACTGATGGAAGGACTTCGACGACCCAGA 2125
QY 2187 CAGAAACGCTTCTCCGAGCGAGCGTGTCTCTCTTCAGGCTGCGGTGAGGAGAAC 2246
DB 2188 CAGAAACGCTTCTCCGAGCGAGCGTGTCTCTCTTCAGGCTGCGGTGAGGAGAAC 2185
QY 2247 CTCTGCGCTTCTTCCAAAGCTCTCTTCTGCGGTGATGCAAGAGACTTCGTGTTGCC 2306
DB 2248 CTCTGCGCTTCTTCCAAAGCTCTCTTCTGCGGTGATGCAAGAGACTTCGTGTTGCC 2245
QY 2307 GCAGTACACTGATGAACTCCACGCGGTGCGCCCTTGTAAACAAACGAAAGCTTAAG 2366
DB 2308 GCAGTACACTGATGAACTCCACGCGGTGCGCCCTTGTAAACAAACGAAAGCTTAAG 2305
QY 2367 CATTCGCCACTTTAGCTG 2383
DB 2368 CATTCGCCACTTTAGCTG 2322
```

RESULT 5

AAS15346

ID AAS15346 standard; cDNA; 3083 BP.

XX AAS15346;

XX 13-FEB-2002 (first entry)

XX

XX

DE DNA encoding human Interleukin 17 (hIL-17) receptor like protein.

XX

KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;

KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;

KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;

KW vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;

KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;

KW bone disease; vascular disorder; eye disorder; cancer; human; ss.

XX Homo sapiens.

XX

XX Location/Qualifiers

XX 22..2235

XX /*tag= a

XX /product= "Interleukin 17 (IL-17) receptor like protein"

XX /partial

XX

XX

XX

XX

XX

XX

XX

Db 1 ATGGCCCGTGGCTGACGCTCTGCTCCGCTCTTCTTAAOGTCAACGCGCTGCTCAACGGC 60
Qy 146 TCGAGCTGGCTGTGGCGCTGGGGGTCCGGCGCGCGCGGGCGCGACACCTGTGGC 205
Db 61 TCGAGCTGGCTGTGGCGCTGGGGGTCCGGCGCGCGGGCGCGACACCTGTGGC 120
Qy 206 TGGAGGATGAAGACGGCTGCCCGACCCCGGCTTGTGTGTCTAATGAGGAGTGGGGCCA 265
Db 121 TGGAG-----GGGAGTGGGGCCA 138
Qy 266 GCCAGCAGAAACAGTGGGCTGTACAACATCACTTCAAATATGACAAATGTACCACTTAC 325
Db 139 GCCAGCAGAAACAGTGGGCTGTACAACATCACTTCAAATATGACAAATGTACCACTTAC 198
Qy 326 TTGAATCCAGTGGGGAAGCATGTGATTCCTGACGCCAGAAATATACCATCAGCCAGTAT 385
Db 199 TTGAATCCAGTGGGGAAGCATGTGATTCCTGACGCCAGAAATATACCATCAGCCAGTAT 258
Qy 386 GCTTGCCATGACCAAGTGGCAGTCAACATCTTTTGGTCCCAGGGGCCCTCGGCATCGAA 445
Db 259 GCTTGCCATGACCAAGTGGCAGTCAACATCTTTTGGTCCCAGGGGCCCTCGGCATCGAA 318
Qy 446 TTCTGAAAGGATTTCCGGTAAATCTGAGAGAGCTGAAAGTCGAGGGGAAGACAGTGCCAA 505
Db 319 TTCTGAAAGGATTTCCGGTAAATCTGAGAGAGCTGAAAGTCGAGGGGAAGACAGTGCCAA 378
Qy 506 CAACGTATCTAAGGATCCGAAGCATCAACAGTACAGTCTCAAGAGTCTGGAATGGA 565
Db 379 CAACGTATCTAAGGATCCGAAGCATCAACAGTACAGTCTCAAGAGTCTGGAATGGA 438
Qy 566 TCTCAACCTTTCCGTAATGAAATTTGAAACGGATTAATTTCTGTAAGGTTGTCCCTTTT 625
Db 439 TCTCAACCTTTCCGTAATGAAATTTGAAACGGATTAATTTCTGTAAGGTTGTCCCTTTT 498
Qy 626 CTTTCCATTAAGAACGAAAGCAATPACACCTTTCTTTTGAACCCGAGCCTGTGAC 685
Db 499 CTTTCCATTAAGAACGAAAGCAATPACACCTTTCTTTTGAACCCGAGCCTGTGAC 558
Qy 686 CTGTTGTTACAGCCGGCAATCTAGCTTGTAAACCTTCTGGAAGCCTCGGAACCTGNAAC 745
Db 559 CTGTTGTTACAGCCGGCAATCTAGCTTGTAAACCTTCTGGAAGCCTCGGAACCTGNAAC 618
Qy 746 ATCAGCCAGCATGGCTCGGACATGAGGTGTCTTCGACCATGACCCGCAACACTTCGGC 805
Db 619 ATCAGCCAGCATGGCTCGGACATGAGGTGTCTTCGACCATGACCCGCAACACTTCGGC 678
Qy 806 TTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACC 865
Db 679 TTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACC 738
Qy 866 TGTAAAGCAGGAGCAAACTACAGAGACGACCGCTCTTCAAAATGTTTCTCCAGGG 925
Db 739 TGTAAAGCAGGAGCAAACTACAGAGACGACCGCTCTTCAAAATGTTTCTCCAGGG 798
Qy 926 GATTATATAATTGAGCTGGTGATGACACTAAACAAAGAAAAGTATGATATATGTC 985
Db 799 GATTATATAATTGAGCTGGTGATGACACTAAACAAAGAAAAGTATGATATATGTC 858
Qy 986 TTAAGCCAGTGCACTCCCGTGGGCGGGGCCATCAGAGCCGTGGCCATCAGAGTGCCA 1045
Db 859 TTAAGCCAGTGCACTCCCGTGGGCGGGGCCATCAGAGCCGTGGCCATCAGAGTGCCA 918
Qy 1046 CTGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCGGCAAGAACCA 1105
Db 919 CTGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCGGCAAGAACCA 978
Qy 1106 GAAATATATATTCACTTTAGTGAAGAGAGCTCTGAGTCTTCACATACACTGCGACA 1165
Db 979 GAAATATATATTCACTTTAGTGAAGAGAGCTCTGAGTCTTCACATACACTGCGACA 1038
Qy 1166 CTCCAGAGAGAGGCTCCGCGCGCGCGAGGCTTTTCTGCTATTCAGTAAAGAT 1225
Db 1039 CTCCAGAGAGAGGCTCCGCGCGCGCGAGGCTTTTCTGCTATTCAGTAAAGAT 1098

Qy 1226 GGCCAGAAATCACATGAATGTCTCAGTGTTCGCTTACTTCTCCAGGACTTCTGTGGC 1285
Db 1099 GGCCAGAAATCACATGAATGTCTCAGTGTTCGCTTACTTCTCCAGGACTTCTGTGGC 1158
Qy 1286 TGTGAGTGGCTCTGGACCTGTGGAAAGACTTCAAGCTCTGTAGAGAAAGGCGCAGAGAA 1345
Db 1159 TGTGAGTGGCTCTGGACCTGTGGAAAGACTTCAAGCTCTGTAGAGAAAGGCGCAGAGAA 1218
Qy 1346 TGGGTCAATCAGAAGATCCAGAGTCCAGTTCATCATTTGTGTTTGTTCAAAAGTATG 1405
Db 1219 TGGGTCAATCAGAAGATCCAGAGTCCAGTTCATCATTTGTGTTTGTTCAAAAGTATG 1278
Qy 1406 AAGTACTTTTGGACAAAGAAAGAACTACAAAACAAAAGAGTGGCCGAGGCTCCGGGAAA 1465
Db 1279 AAGTACTTTTGGACAAAGAAAGAACTACAAAACAAAAGAGTGGCCGAGGCTCCGGGAAA 1338
Qy 1466 GGAGAGCTCTTCTTGGTGGGGTGTGAGCCATTGCCGAAAGCTCCGCGAGGCGCAAGCAG 1525
Db 1339 GGAGAGCTCTTCTTGGTGGGGTGTGAGCCATTGCCGAAAGCTCCGCGAGGCGCAAGCAG 1398
Qy 1526 AGTTTGGTCCGGGGCTCAGCAAGTTTATCGCGCTCTACTTTGATTATTTCTGCGAGGGA 1585
Db 1399 AGTTTGGTCCGGGGCTCAGCAAGTTTATCGCGCTCTACTTTGATTATTTCTGCGAGGGA 1458
Qy 1586 GAGCTCCCGGCTATCTTAGACCTGAGTACCAAGTACAGACTCATGGACAATC-TTCTCTCA 1644
Db 1459 GAGCTCCCGGCTATCTTAGACCTGAGTACCAAGTACAGACTCATGGACAATC-TTCTCTCA 1518
Qy 1645 GCTCTGTTCCCACT-TGCACTCCCGAGACCAAGCTTCCAGGAGCCGGGCA-GCAACAG 1702
Db 1519 GCTCTGTTCCCACTCTGCACTCCCGAGACCAAGCTTCCAGGAGCCGGGCAAGCAGCAG 1578
Qy 1703 CGACAGGGCA-GCAGAAGGAACACTTTCGAGGCAAGTCAAGGCGGCTCCCTATACGTCGC 1761
Db 1579 CGACAGGGCAAGGAAGAACTACTTTCGAGAGCAAGTCAAGGCGGCTCCCTATACGTCGC 1638
Qy 1762 CATTTGCAACATGACCAAGCTTTATTGACAGAGGAGCCGACCTGCTTTCGAAAGAGAGTTCGT 1821
Db 1639 CATTTGCAACATGACCAAGCTTTATTGACAGAGGAGCCGACCTGCTTTCGAAAGAGAGTTCGT 1698
Qy 1822 TCCCTTCCATCTCTCTCCACTGCGCTACCGGGAGCCAGTCTTTGAGAGAAATTTGATTCGGG 1881
Db 1699 TCCCTTCCATCTCTCTCCACTGCGCTACCGGGAGCCAGTCTTTGAGAGAAATTTGATTCGGG 1758
Qy 1882 CTTGGTTTAAAATGATGTATGTGCAAAACAGGGCCCTGAGAGTCACTTCTGCTTAAAGGT 1941
Db 1759 CTTGGTTTAAAATGATGTATGTGCAAAACAGGGCCCTGAGAGTCACTTCTGCTTAAAGGT 1818
Qy 1942 AGAGCGGCTGTTCTTTCGGGCAACCGGACCAAGCCGACCTCCAGCAGCAGAGTCAAGCATGG 2001
Db 1819 AGAGCGGCTGTTCTTTCGGGCAACCGGACCAAGCCGACCTCCAGCAGCAGAGTCAAGCATGG 1878
Qy 2002 GGGCTTGAGCAAGACAGCGGGAGGCGCGGCTTGCCTTTGACGGTAGCGCGCTTGCACACC 2061
Db 1879 GGGCTTGAGCAAGACAGCGGGAGGCGCGGCTTGCCTTTGACGGTAGCGCGCTTGCACACC 1938
Qy 2062 CTTGCTGACACGSGTGAAGCGCGCAGCCCTCGGACATGCGCGGGGACTCAGGCACTA 2121
Db 1939 CTTGCTGACACGSGTGAAGCGCGCAGCCCTCGGACATGCGCGGGGACTCAGGCACTA 1998
Qy 2122 TGACTCTGTGCGCCCTCATCCGAGCTGTCTCTCCACTGATGGAAGAGCTCTCGACGGA 2181
Db 1999 TGACTCTGTGCGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGAGCTCTCGACGGA 2058
Qy 2182 CCAGACAGAAACGCTTTCCCTGACGAGAGCGTCTCTCTTTTTCAGGCTTGGGTGAGGA 2241
Db 2059 CCAGACAGAAACGCTTTCCCTGACGAGAGCGTCTCTCTCTTTTTCAGGCTTGGGTGAGGA 2118
Qy 2242 GGAACCTTCTGCGCTTCTTCCAAAGCTCTCTCTTCTGGGTGATGCAAGAGAGTCTTGG 2301
Db 2119 GGAACCTTCTGCGCTTCTTCCAAAGCTCTCTCTTCTGGGTGATGCAAGAGAGTCTTGG 2178

| | | | |
|----|------|---|------|
| Qy | 2302 | TTGCCGAGCTACACTGATGAACTCCACGCGGTGCGCCCTTTGTAAACAAACGAAAGT | 2361 |
| Db | 2179 | TTGCCGAGCTACACTGATGAACTCCACGCGGTGCGCCCTTTGTAAACAAACGAAAGT | 2238 |
| Qy | 2362 | CTAAGCATTTGCCACTTTAGCTG | 2383 |
| Db | 2239 | CTAAGCATTTGCCACTTTAGCTG | 2260 |

| | |
|----------|---|
| RESULT 7 | |
| ADB63275 | |
| ID | ADB63275 standard; cDNA; 2894 BP. |
| XX | |
| XX | |
| AC | ADB63275; |
| XX | |
| XX | 04-DEC-2003 (first entry) |
| XX | |
| DE | Human cDNA encoding clone TESTI20046540. |
| XX | |
| KW | Human; ss; gene; pharmaceutical; diagnostic; gene therapy; |
| KW | tissue regeneration; cell regeneration; membrane protein; |
| KW | signal transduction-related protein; transcription-related protein; |
| KW | osteoporosis; neurological disease; cancer; tumour. |
| XX | |
| OS | Homo sapiens. |

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FT /tag= a
FT /product= "Clone TESTI20046540 protein"
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| | |
|----|---|
| CC | encoding them can be used as indicators for diseases (e.g. osteoporosis, |
| CC | neurological diseases, cancer, tumours. The cDNA may be used to regulate |
| CC | the activity or expression of the encoded protein to treat diseases. The |
| CC | sequence presented is a cDNA of the invention. Note: Some of the sequence |
| CC | data for this patent is not represented in the printed specification, but |
| CC | is based on sequence information supplied by the European Patent Office. |
| XX | |
| SQ | Sequence 2894 BP; 735 A; 751 C; 730 G; 678 T; 0 U; 0 Other; |
| | |
| | Query Match 89.3%; Score 2128; DB 10; Length 2894; |
| | Best Local Similarity 98.6%; Pred. No. 0; |
| | Matches 2146; Conservative 0; Mismatches 30; Indels 0; Gaps 0; |
| QY | 208 GAGATGAAGAAGCGGCTGCCGACCCCGGCTTTGTGTTCATAATGAGGGAGTGGGGCAGC 267 |
| DB | 170 GTGGCTCAAAAGTGTGGCTGCACTACAGGCACAATCCTGGCCCTTGGCAGGGAGTGGGGCCAGC 229 |
| QY | 268 CAGCAGAAACAGTGGGCTGTACAACTCACCTTCAAATATGCAATTTGTACCACCTACTT 327 |
| DB | 230 CAGCAGAAACAGTGGGCTGTACAACTCACCTTCAAATATGCAATTTGTACCACCTACTT 289 |
| QY | 328 GAATCCAGTGGGGAAGCATGTGATTGCTGACGCCAAGAATATCACCATCAGCCAGATATGC 387 |
| DB | 290 GAATCCAGTGGGGAAGCATGTGATTGCTGACGCCAAGAATATCACCATCAGCCAGATATGC 349 |
| QY | 388 TTGCCATGACCAAGTGCGAGTCACCAATTTCTTTGGTCCCCAGGGGCCCTCGGCATTCGAATT 447 |
| DB | 350 TTGCCATGACCAAGTGCGAGTCACCAATTTCTTTGGTCCCCAGGGGCCCTCGGCATTCGAATT 409 |
| QY | 448 CCTGAAGAAGTAATTCGGGTAACTACTGGAGGAGCTGNAAGTCGGAGGGAGAGCAGTGCCAAC 507 |
| DB | 410 CCTGAAGAAGTAATTCGGGTAACTACTGGAGGAGCTGNAAGTCGGAGGGAGAGCAGTGCCAAC 469 |
| QY | 508 ACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAAGAACTCGAATGGAATC 567 |
| DB | 470 ACTGATTCTAAAGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAAGAACTCGAATGGAATC 529 |
| QY | 568 TCACCTTTTCTCGAATATGAAATTTGAAACCGGATTAATTCGTAAAGGTTGTCCCTTTTTCC 627 |
| DB | 530 TCACCTTTTCTCGAATATGAAATTTGAAACCGGATTAATTCGTAAAGGTTGTCCCTTTTTCC 589 |
| QY | 628 TTCATTAATAAAA CGAAGAGCAATTACACACCTTTCTCTTTAGAACCCGAGCCTGTGACCT 687 |
| DB | 590 TTCATTTAAAAA CGAAGAGCAATTTACCAACCTTTCTCTTTTAGAACC CGAGCCTGTGACCT 649 |
| QY | 688 GTTGTTACAGCCGACAACTAGCTTGTCTAAACCTCTCTGGAAGCCTCGGAACCTGGAACAT 747 |
| DB | 650 GTTGTTACAGCCGACAACTTAGCTTTGTAAACCTCTCTGGAAGCCTCGGAACCTGGAACAT 709 |
| QY | 748 CAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCACCGCACAACTTCGGCTT 807 |
| DB | 710 CAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCACCGCACAACTTCGGCTT 769 |
| QY | 808 CCGTTTCTTCTATCTTCACATCAAGCTCAAGCAGGAAGGACCTTTCAAGCGGAAGACCTG 867 |
| DB | 770 CCGTTTCTTCTATCTTCACATCAAGCTCAAGCAGGAAGGACCTTTCAAGCGGAAGACCTG 829 |
| QY | 868 TAAGCAGGACCAACTACAGAGCGACCGAGCTGCTCTTCAAAAATGTTTCTCCAGGGGA 927 |
| DB | 830 TAAGCAGGAGCAACTACAGAGATGACCAAGCTGCTCTTCAAAAATGTTTCTCCAGGGGA 889 |
| QY | 928 TTATATAATTGAGCTGGTGGATGACACTAAACAACAAGAAAAAGTGTGATTCATTTATGCTT 987 |
| DB | 890 TTATATAATTGAGCTGGTGGATGACACTTAACADACAAAGAAAGTGTGATTCATTTATGCTT 949 |
| QY | 988 AAAGCCAGTGCACTCCCGCTGGGCCGGCCCAATCAGAGCCGTGGCCAATCAAGTGCCACT 1047 |
| DB | 950 AAAGCCAGTGCACTCCCGCTGGGCCGGGCCCAATCAGAGCCGTGGCCAATCAAGTGCCACT 1009 |
| QY | 1048 GGTTAGTCATATCGCAATTCGGCGAGCTCTTCACTGTGATGTGCCGGAAGCAACAAGA 1107 |
| DB | 1010 GGTTAGTCATATCGGCAATTCGGCGAGCTCTTCACTGTGATGTGCCGGAAGCAACAAGA 1069 |

Qy 1108 AAATATATATTTACATTTAGATGAAGAGAGCTCTGAGTCTTTCCACATACACTGCAGCACT 1167
Db 1070 AAATATATATTTACATTTAGATGAAGAGAGCTCTGAGTCTTTCCACATACACTGCAGCACT 1129
Qy 1168 CCCAAGAGAGAGGCTCCGGCCCGCCGCGAAGGTCTTTCTCTGCTATTTCCAGTAAGATGG 1227
Db 1130 CCCAAGAGAGAGGCTCCGGCCCGCCGCGAAGGTCTTTCTCTGCTATTTCCAGTAAGATGG 1189
Qy 1228 CCAGNATCACATGAATGTCGTCAGTGTTCGCTTACTTCTCCAGNACTTCTGTGGCTG 1287
Db 1190 CCAGNATCACATGAATGTCGTCAGTGTTCGCTTACTTCTCCAGNACTTCTGTGGCTG 1249
Qy 1288 TGAGTGGCTCTGGACCTGTGGGAAGACTTCAGGCTCTGTAGAGAAGGCGAGAGAAATG 1347
Db 1250 TGAGTGGCTCTGGACCTGTGGGAAGACTTCAGGCTCTGTAGAGAAGGCGAGAGAAATG 1309
Qy 1348 GGTCAATCAGAAGATCCAGAGTCCAGTTCATCATTTGCTGTTTGTTCCAAAGGTATGAA 1407
Db 1310 GGTCAATCAGAAGATCCAGAGTCCAGTTCATCATTTGCTGTTTGTTCCAAAGGTATGAA 1369
Qy 1408 GTACTTTGTGACAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCGGGGAAGG 1467
Db 1370 GTACTTTGTGACAAGAACTACAAACACAAAGGAGGTGGCCGAGGCTCGGGGAAGG 1429
Qy 1468 AGAGCTCTTCTGTGGGGTGTGAGCCATTTGCCGAAAAGCTCCGCCAGGCGCAAGCAGAG 1527
Db 1430 AGAGCTCTTCTGTGGGGTGTGAGCCATTTGCCGAAAAGCTCCGCCAGGCGCAAGCAGAG 1489
Qy 1528 TTGCTCCGCGGCGCTCAGCAAGTTTATCGCGGTCTACTTTGATTTATCTCTCGAGGGAGA 1587
Db 1490 TTGCTCCGCGGCGCTCAGCAAGTTTATCGCGGTCTACTTTGATTTATCTCTCGAGGGAGA 1549
Qy 1588 CGTCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGAGCAATCTTCTCAGCT 1647
Db 1550 CGTCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGAGCAATCTTCTCAGCT 1609
Qy 1648 CTGTTCCCACTTGCACTCCGAGACCAAGGCTCCAGGAGCGGGGAGCAGACACGCGACA 1707
Db 1610 CTGTTCCCACTTGCACTCCGAGACCAAGGCTCCAGGAGCGGGGAGCAGACACGCGACA 1669
Qy 1708 GGGCAGCAGAAAGGAATCTATTTCCGAGCAAGTCAAGCGGTCCTTATACGTCGCCATTTG 1767
Db 1670 GGGCAGCAGAAAGGAATCTATTTCCGAGCAAGTCAAGCGGTCCTTATACGTCGCCATTTG 1729
Qy 1768 CAACATGACACAGATTTATGACGAGGAGCCCGAATGGTTCGAAAAGCAGTTCTCCCTT 1827
Db 1730 CAACATGACACAGATTTATGACGAGGAGCCCGAATGGTTCGAAAAGCAGTTCTCCCTT 1789
Qy 1828 CCATCCTCTCCACTCGGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGT 1887
Db 1790 CCATCCTCTCCACTCGGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGT 1849
Qy 1888 TTTAAATGATGTGATGTCAAAACCAAGGCTCGAGAGTACTTCTGCTTAAAGGTAGAGGC 1947
Db 1850 TTTAAATGATGTGATGTCAAAACCAAGGCTCGAGAGTACTTCTGCTTAAAGGTAGAGGC 1909
Qy 1948 GGCTGTTCTTGGGGCAACCGGACCGCGACTCCAGCAGCAGAGTCAAGCATGGGGGCT 2007
Db 1910 GGCTGTTCTTGGGGCAACCGGACCGCGACTCCAGCAGCAGAGTCAAGCATGGGGGCT 1969
Qy 2008 GGACCCAGACGGGGAGGCCCGGCTGCTTGAAGGTAGCGCCGCTGCAACCCCTGCT 2067
Db 1970 GGACCCAGACGGGGAGGCCCGGCTGCTTGAAGGTAGCGCCGCTGCAACCCCTGCT 2029
Qy 2068 GCACACGGTGAAGCCGCGAGCCCTCCGACATGCGCGGAGTCAAGGCATCTATGACTC 2127
Db 2030 GCACACGGTGAAGCCGCGAGCCCTCCGACATGCGCGGAGTCAAGGCATCTATGACTC 2089
Qy 2128 GTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTTCGACGGAACAGAC 2187
Db 2090 GTCTGTGCCCTCATCCGAGCTGTCTCTGCCACTGATGGAAGGACTCTTCGACGGAACAGAC 2149
Qy 2188 AGAAACGCTTTCCTGACGGAGAGCGTGTCTCTCTTTCAGGCTGGGTGAGGAGAAC 2247

Db 2150 AGAAACGCTTTCCTGACGGAGAGCGTGTCTCTCTTTCAGGCTGGGTGAGGAGAAC 2209
Qy 2248 TCCGTGCCCTTCTTCCAAAGCTCTCTCTTCTGGGTGATGCAAAACAGATCTTGTGTGCCG 2307
Db 2210 TCCGTGCCCTTCTTCCAAAGCTCTCTCTTCTGGGTGATGCAAAACAGATCTTGTGTGCCG 2269
Qy 2308 CAGCTACACTGATGAATCTCCAGCGGTCGCCCCCTTTGTAAACAAACGAAAGAGTCTAAGC 2367
Db 2270 CAGCTACACTGATGAATCTCCAGCGGTCGCCCCCTTTGTAAACAAACGAAAGAGTCTAAGC 2329
Qy 2368 ATTGCCACTTTAGCTG 2383
Db 2330 ATTGCCACTTTAGCTG 2345

RESULT 8
ABX71363
ID ABX71363 standard; cDNA; 2406 BP.
XX AC ABX71363;
XX AC
XX 14-APR-2003 (first entry)
XX Human transmembrane protein cDNA from clone DKF2phtes3_2013.
XX Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
XX Homo sapiens.
XX OS
XX WO200112659-A2.
XX 22-FEB-2001.
XX 18-AUG-2000; 2000WO-IB001496.
XX 18-AUG-1999; 99US-0149499P.
XX 28-SEP-1999; 99US-0156503P.
XX (GSHU-) GERMAN HUMAN GENOME PROJECT.
XX Wiemann S;
XX WPI; 2001-327840/34.
XX P-PSDB; ABUS3091.
XX Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
XX Claim 1; Page 698; 1095pp; English.
XX This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention
XX Sequence 2406 BP; 633 A; 650 C; 589 G; 534 T; 0 U; 0 Other;
SQ

Query Match 89.3%; Score 2127.2; DB 5; Length 2406;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2129; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 252 AGGAGTGGGGCCAGCCAGCAGAGAAACAGTGGGCTGTACAAACATCACCCTTCAAAATATGACA 311
Db 38 AGGAGTGGGGCCAGCCAGCAGAGAAACAGTGGGCTGTACAAACATCACCCTTCAAAATATGACA 97
Qy 312 ATTGTACCACCTACTTGAATTCAGTGGGGAAGCATGTGATTGCTGAGCCGCCAGAAATATCA 371

Db 98 ATGTGACCACTACTTGAATCGAGTGGGGAAGCATGTGATTTGCTGACGCCGAGAAATATCA 157
Qy 372 CCATCAGCCAGTATGCTCTGATGCCATGACCAAGTGGCAGTCAACATTTCTTTGGTCCCGAGGG 431
Db 158 CCATCAGCCAGTATGCTCTGATGCCATGACCAAGTGGCAGTCAACATTTCTTTGGTCCCGAGGG 217
Qy 432 CCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG 491
Db 218 CCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG 277
Qy 492 GAAGCAGTGCACAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551
Db 278 GAAGCAGTGCACAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 337
Qy 552 GAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGAATATTTCGTAA 611
Db 338 GAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGAATATTTCGTAA 397
Qy 612 AGGTTGTCCCTTTCCCTTCAATAAAGCAATTTACACCTTTCTTTTAGAA 671
Db 398 AGGTTGTCCCTTTCCCTTCAATAAAGCAATTTACACCTTTCTTTTAGAA 457
Qy 672 CCCGAGCCTGTGACCTGTTGTTACAGCCGAGCAATCTAGCTTGTAAACCTTCTGGAAGC 731
Db 458 CCCGAGCCTGTGACCTGTTGTTACAGCCGAGCAATCTAGCTTGTAAACCTTCTGGAAGC 517
Qy 732 CTCGGAACCTGAAATCAGCAGCATGCTCGGACATGCAAGTGTCTTTGACACATGAC 791
Db 518 CTCGGAACCTGAAATCAGCAGCATGCTCGGACATGCAAGTGTCTTTGACACATGAC 577
Qy 792 CGCAAACTTCGGCTTCGGTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTT 851
Db 578 CGCAAACTTCGGCTTCGGTTCTTCTATCTTCACTACAAGCTCAAGCAGCAAGGACCTT 637
Qy 852 TCAAGCGAAAGCCTGTGAAGCAGGAGCAAACTACAGAGAGCAGCTGCCTCTCTCAA 911
Db 638 TCAAGCGAAAGCCTGTGAAGCAGGAGCAAACTACAGAGAGCAGCTGCCTCTCTCAA 697
Qy 912 ATGTTTCTCCAGGGAATATATAATTTGAGCTGGTGAGTGAACAACAACAAG 971
Db 698 ATGTTTCTCCAGGGAATATATAATTTGAGCTGGTGAGTGAACAACAACAAG 757
Qy 972 TGATGATTTATGCTTAAAGCAGTGCATCTCCCGTGGGCCGCGCCATCAGAGCCGTGG 1031
Db 758 TGATGATTTATGCTTAAAGCAGTGCATCTCCCGTGGGCCGCGCCATCAGAGCCGTGG 817
Qy 1032 CCATCAGTGCCTGCTGATGATCATATCGGCATTCGCGAGCTCTTCACTGTGATGCC 1091
Db 818 CCATCAGTGCCTGCTGATGATCATATCGGCATTCGCGAGCTCTTCACTGTGATGCC 877
Qy 1092 GCAAGAGCAACAAGAAATATATATTACATTTAGATGAAGAGCTCTGAGTCTTCCA 1151
Db 878 GCAAGAGCAACAAGAAATATATATTACATTTAGATGAAGAGCTCTGAGTCTTCCA 937
Qy 1152 CATACACTGACACTCTCCCAAGAGAGGCTCCGCGCGCGCGGAGGCTTTCTCTGCT 1211
Db 938 CATACACTGACACTCTCCCAAGAGAGGCTCCGCGCGCGCGGAGGCTTTCTCTGCT 997
Qy 1212 ATTCAGTAAGATGCCAGAAATCATGAATGTGCTCGAGTGTTCGCTACTTCTCTCC 1271
Db 998 ATTCAGTAAGATGCCAGAAATCATGAATGTGCTCGAGTGTTCGCTACTTCTCTCC 1057
Qy 1272 AGGACTTCTGTGGTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAG 1331
Db 1058 AGGACTTCTGTGGTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAG 1117
Qy 1332 AAGGCGAGAGAGTGGGTCTATCCAGAGATCCAGAGTCCAGTTCATCATTTGGTTT 1391
Db 1118 AAGGCGAGAGAGTGGGTCTATCCAGAGATCCAGAGTCCAGTTCATCATTTGGTTT 1177
Qy 1392 GTTCCAAAGGTTATGAAGTACTTTGTGGAACAAGAGAACTTACAAACACAAGAGGTGGCC 1451

Db 1178 GTTCCAAAGGTTATGAAGTACTTTTGGACAGAAGAACTACAAACACAAGAGGTGGCC 1237
Qy 1452 GAGGCTCGGGAAAGGAGAGCTCTTCTGTGTGGGGTGTGAGCCATTTGCCGAAAAGCTGCC 1511
Db 1238 GAGGCTCGGGAAAGGAGAGCTCTTCTGTGTGGGGTGTGAGCCATTTGCCGAAAAGCTGCC 1297
Qy 1512 GCGAGGCCAAGCAGAGTTGCTTCGGGGGCTCAGCAAGTTTATCGCCCTTACTTTGATT 1571
Db 1298 GCGAGGCCAAGCAGAGTTGCTTCGGGGGCTCAGCAAGTTTATCGCCCTTACTTTGATT 1357
Qy 1572 ATTCTGCGAGGAGAGCTGCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGG 1631
Db 1358 ATTCTGCGAGGAGAGCTGCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGG 1417
Qy 1632 ACAATCTTCTCAGCTCTGTTTCCCACTTTCGACCTCCCGAGACACAGGCTTCAGAGAGCGG 1691
Db 1418 ACAATCTTCTCAGCTCTGTTTCCCACTTTCGACCTCCCGAGACACAGGCTTCAGAGAGCGG 1477
Qy 1692 GCGAGCACCGGACAGGCGAGCAAGAACTACTTCCGGAGCAAGTCAAGCCCGTCCC 1751
Db 1478 GCGAGCACCGGACAGGCGAGCAAGAACTACTTCCGGAGCAAGTCAAGCCCGTCCC 1537
Qy 1752 TATAGCTCGCATTTGCAACATGCAACAGTATTATTAGCAGAGAGCCCGACTGTTTCGAAA 1811
Db 1538 TATAGCTCGCATTTGCAACATGCAACAGTATTATTAGCAGAGAGCCCGACTGTTTCGAAA 1597
Qy 1812 AGCAGTTGCTTCCCTTCCATCTCTCCACTGCGCTACCGGGAGCCAGTCTTTGGAGAAAT 1871
Db 1598 AGCAGTTGCTTCCCTTCCATCTCTCCACTGCGCTACCGGGAGCCAGTCTTTGGAGAAAT 1657
Qy 1872 TTGATTCCGGCTTGGTTTAAATGATGTGCAAAACCGAGGCTGAGAGTACTTCT 1931
Db 1658 TTGATTCCGGCTTGGTTTAAATGATGTGCAAAACCGAGGCTTGAAGTACTTCT 1717
Qy 1932 GCCTAAAGTAGAGCGGCTGTTCTTGGGGCAACCGGACCGAGCTCCCAAGCAGAGA 1991
Db 1718 GCCTAAAGTAGAGCGGCTGTTCTTGGGGCAACCGGACCGAGCTCCCAAGCAGAGA 1777
Qy 1992 GTCAGACTGGGGGCTCGACCAAGACGGGAGGCGCGGCTTCCCTTGAAGTGGAGGAC 2051
Db 1778 GTCAGACTGGGGGCTCGACCAAGACGGGAGGCGCGGCTTCCCTTGAAGTGGAGGAC 1837
Qy 2052 CCCTGCAACCCCTGCTGACAGGTTGAAGCGGAGCGGCGGCTTCGACATGCCCGGAGCT 2111
Db 1838 CCCTGCAACCCCTGCTGACAGCGGTGAAGCGGAGCGGCGGCTTCGACATGCCCGGAGCT 1897
Qy 2112 CAGGACTATGACTGCTGTCCTCATCCGAGCTGTCTCTGCGCACTGATGGAAGGAC 2171
Db 1898 CAGGACTATGACTGCTGTCCTCATCCGAGCTGTCTCTGCGCACTGATGGAAGGAC 1957
Qy 2172 TCTCGACGGACCAAGCAAGAAAGCTTCTCCCTGACGGAGAGCGTCTCTCTTCAGGCC 2231
Db 1958 TCTCGACGGACCAAGCAAGAAAGCTTCTCCCTGACGGAGAGCGTCTCTCTTCAGGCC 2017
Qy 2232 TGGGTGAGAGGAACTCTCTGCGCTTCTTCCAGCTCTCTCTTCTTCTGCGGTATGCAAG 2291
Db 2018 TGGGTGAGAGGAACTCTCTGCGCTTCTTCCAGCTCTCTCTTCTTCTGCGGTATGCAAG 2077
Qy 2292 CAGATCTTGGTTCGCGAGCTACACTGATGAACCTCCAGCGGCTCGCCCTTTGTAAACAA 2351
Db 2078 CAGATCTTGGTTCGCGAGCTACACTGATGAACCTCCAGCGGCTCGCCCTTTGTAAACAA 2137
Qy 2352 ACGAAAGAGTCTAAGCATTTGCCATTTAGCTG 2383
Db 2138 ACGAAAGAGTCTAAGCATTTGCCATTTAGCTG 2169

RESULT 9

AAS09517

ID AAS09517 standard; cdna; 2319 BP.

XX

AAS09517;

XX

| | | | | | | | |
|----|--|---|-----------------------|--|---------------|------------|--------------|
| DT | 24-OCT-2001 | (first entry) | Query Match | 87.0%; | Score 2074.2; | DB 4; | Length 2319; |
| XX | Human cDNA encoding Interleukin 17 receptor, IL-17RH4. | | Best Local Similarity | 98.1%; | Pred. No. 0; | | |
| DE | | | Matches 2125; | Conservative | 0; | Mismatches | 3; |
| XX | | | | | | Indels | 39; |
| XX | | | | | | Gaps | 1; |
| KW | Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; ss; | | 252 | AGGAGTGGGCGCAGCAGAGAAACAGTGGGTGTACAAACATCATCCTTCAATATGACA | 311 | | |
| KW | PRO20026; DNA 154095-2998; systemic lupus erythematosus; | | 122 | AGGAGTGGGCGCAGCAGAGAAACAGTGGGTGTACAAACATCATCCTTCAATATGACA | 181 | | |
| KW | rheumatoid arthritis; osteoarthritis; diabetes mellitus; | | 312 | ATTGTACCACTACTTGAATCCAGTGGGGAAGCATGTGTTGCTGAGCCGAGAAATATCA | 371 | | |
| KW | allergic disease; asthma; demyelinating disease; | | 182 | ATTGTACCACTACTTGAATCCAGTGGGGAAGCATGTGTTGCTGAGCCGAGAAATATCA | 241 | | |
| XX | degenerative cartilaginous disorder; transplantation associated disease. | | | | | | |
| OS | Homo sapiens. | | | | | | |
| XX | | Key | 70. | 2255 | | | |
| XX | | Location/Qualifiers | | | | | |
| XX | | CDS | | | | | |
| XX | | /*tag= a | | | | | |
| XX | | /product= "IL-17RH4" | | | | | |
| XX | | WO200146420-A2. | | | | | |
| XX | | 28-JUN-2001. | | | | | |
| XX | | 20-DEC-2000; 2000WO-US034956. | | | | | |
| XX | | 23-DEC-1999; 99US-0172096P. | | | | | |
| XX | | 30-DEC-1999; 99WO-US031274. | | | | | |
| XX | | 11-JAN-2000; 2000US-0175481P. | | | | | |
| XX | | 18-FEB-2000; 2000WO-US004341. | | | | | |
| XX | | 02-MAR-2000; 2000WO-US005841. | | | | | |
| XX | | 21-MAR-2000; 2000US-0191007P. | | | | | |
| XX | | 02-JUN-2000; 2000WO-US015264. | | | | | |
| XX | | 22-JUN-2000; 2000US-0213807P. | | | | | |
| XX | | 22-AUG-2000; 2000US-00644848. | | | | | |
| XX | | 24-AUG-2000; 2000WO-US023328. | | | | | |
| XX | | 24-OCT-2000; 2000US-0242837P. | | | | | |
| XX | | 10-NOV-2000; 2000WO-US030873. | | | | | |
| XX | | 28-NOV-2000; 2000US-0253646P. | | | | | |
| XX | | 01-DEC-2000; 2000WO-US032678. | | | | | |
| XX | | (GETH) GENENTECH INC. | | | | | |
| XX | | Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ; | | | | | |
| XX | | Gurney AL, Li H, Hillan KJ, Tamas D, Van Lookeren M, Vandlen RL; | | | | | |
| XX | | Watanabe CK, Williams PM, Wood WI, Yansura DG; | | | | | |
| XX | | WPI; 2001-451708/48. | | | | | |
| XX | | P-PSDB; AAU04958. | | | | | |
| XX | | Novel PRO polypeptides homologous to interleukin-17, useful for the | | | | | |
| XX | | diagnosis and treatment of immune related disease e.g. rheumatoid | | | | | |
| XX | | arthritis and diabetes. | | | | | |
| XX | | Claim 1; Fig 17; 188pp; English. | | | | | |
| XX | | The sequence (DNA 154095-2998) encodes a PRO polypeptide (PRO20026) which | | | | | |
| XX | | is the human Interleukin 17 receptor, IL-17RH4. A composition containing | | | | | |
| XX | | antagonists to the PRO polypeptides or individual components are useful | | | | | |
| XX | | for treating a mammal with an immune related disease, e.g. systemic lupus | | | | | |
| XX | | erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic | | | | | |
| XX | | arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic | | | | | |
| XX | | inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, | | | | | |
| XX | | sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, | | | | | |
| XX | | thyroiditis, diabetes mellitus, immune-mediated renal disease, a | | | | | |
| XX | | demyelinating disease, an autoimmune or immune-mediated skin disease, | | | | | |
| XX | | contact dermatitis, an allergic disease e.g. food hypersensitivity, | | | | | |
| XX | | asthma, a transplantation associated disease, or a chronic inflammatory | | | | | |
| XX | | demyelinating polynuropathy. Treating a degenerative cartilaginous | | | | | |
| XX | | disorder comprises administering a PRO1031 or PRO1122 polypeptide | | | | | |
| XX | | agonist, or antagonist to the mammal. Numerous examples of the diseases | | | | | |
| XX | | and disorders are given in the specification | | | | | |
| XX | | Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other; | | | | | |

Db 1142 ATCATGAAATGTCAGTTCAGTTCCTCCAGGACTTCCTGCGCTGTGAGG 1201
QY TGGCTCTGGACCTGTGGGAAGACTTCAGCTCTGTAGAGAGGCGAGAGAAATGGGTCA 1352
Db 1202 TGGCTCTGGACCTGTGGGAAGACTTCAGCTCTGTAGAGAGGCGAGAGAAATGGGTCA 1261
QY TCCAGAACTCCAGAGTCCAGTTCATCATTTGTTGTTTCCAAAGGTATGAAGTACT 1412
Db 1262 TCCAGAACTCCAGAGTCCAGTTCATCATTTGTTGTTTCCAAAGGTATGAAGTACT 1321
QY TTGTGGACAAGAACTTACAAACACAAAGAGGTGGCGGAGTTCGGGGAAAAGAGAGC 1472
Db 1322 TTGTGGACAAGAACTTACAAACACAAAGAGGTGGCGGAGTTCGGGGAAAAGAGAGC 1381
QY TCTTCTGTTGGCGGTGTGAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGCAGAGTTCGT 1532
Db 1382 TCTTCTGTTGGCGGTGTGAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGCAGAGTTCGT 1441
QY CCGGGGCTCAGCAAGTTTATCGCGGTCTACTTTGATTATTCCTGCGAGGAGACGTCC 1592
Db 1442 CCGGGGCTCAGCAAGTTTATCGCGGTCTACTTTGATTATTCCTGCGAGGAGACGTCC 1501
QY CCGGTATCTAGACCTGAGTACCAAGTACAGACTATCGACAACTTCTCAGCTCTGTT 1652
Db 1502 CCGGTATCTAGACCTGAGTACCAAGTACAGACTATCGACAACTTCTCAGCTCTGTT 1561
QY CCCACTTGCATCCGAGACACCGGCTCCAGGAGCGGGGCGAGCACACGCGACAGGGCA 1712
Db 1562 CCCACTTGCATCCGAGACACCGGCTCCAGGAGCGGGGCGAGCACACGCGACAGGGCA 1621
QY GCAGAGAACTACTTCCGAGAGCAAGTCAGCGCGTCCCTATAGTGCCTCATTTGCAACA 1772
Db 1622 GCAGAGAACTACTTCCGAGAGCAAGTCAGCGCGTCCCTATAGTGCCTCATTTGCAACA 1681
QY TGCACAGTTTATTGACGAGGAGCGGCTGTTTGGAAAGAGTTCGTTCCCTTCCATC 1832
Db 1682 TGCACAGTTTATTGACGAGGAGCGGCTGTTTGGAAAGAGTTCGTTCCCTTCCATC 1741
QY CTCTCCACTGCGCTACCGGAGCGAGCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892
Db 1742 CTCTCCACTGCGCTACCGGAGCGAGCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801
QY ATGATGTCATGTGCAAAACAGGGCTGAGAGTGTCTGCTTAAAGGTAGAGGGCGGTG 1952
Db 1802 ATGATGTCATGTGCAAAACAGGGCTGAGAGTGTCTGCTTAAAGGTAGAGGGCGGTG 1861
QY TCTTGGGGCAACCGGACCGGACTCCAGCAGAGAGTCCAGTGGGGGCTTGAGC 2012
Db 1862 TCTTGGGGCAACCGGACCGGACTCCAGCAGAGAGTCCAGTGGGGGCTTGAGC 1921
QY AAGACGGGAGCGCGGCTGCGCTTGAAGTGGCGGCTGCAACCCCTGTGCAACA 2072
Db 1922 AAGACGGGAGCGCGGCTGCGCTTGAAGTGGCGGCTGCAACCCCTGTGCAACA 1981
QY CGGTGAAGCGGAGCGGCTGCGCATGCGCGGACTCAGGCACTATGACTCGTCTG 2132
Db 1982 CGGTGAAGCGGAGCGGCTGCGCATGCGCGGACTCAGGCACTATGACTCGTCTG 2041
QY TGCCCTCATCCAGTGTCTCTGCGCACTGATGGAAGGACTCTCCGACGACACAGAGAAA 2192
Db 2042 TGCCCTCATCCAGTGTCTCTGCGCACTGATGGAAGGACTCTCCGACGACACAGAGAAA 2101
QY CGTCTTCCCTGACGAGAGCGGTCTCTCTTTCAGGCTGGGTGAGAGGAACTCTCTG 2252
Db 2102 CGTCTTCCCTGACGAGAGCGGTCTCTCTTTCAGGCTGGGTGAGAGGAACTCTCTG 2161
QY CCCTTCTTCCAGTCTCTCTCTTTCAGGCTGGGTGAGAGGAACTCTCTG 2312
Db 2162 CCCTTCTTCCAGTCTCTCTCTTTCAGGCTGGGTGAGAGGAACTCTCTG 2221
QY ACACATGATGAACTCCACAGCGGTGCGCCCTTCTTGAACAAAGAGTCTAAGCATTCG 2372

Db 2222 AACTGTATGAACCTCCACGCGTCCGCCCTTTGTAAACAAAGAGTCTAAGCATTCG 2281
QY 2373 CACTTTA 2379
Db 2282 CACTTTA 2288
RESULT 10
ACAB9858
ID ACA89858 standard; cDNA; 2319 BP.
XX ACA89858;
AC ACA89858;
XX
DT 10-JUL-2003 (first entry)
XX
DE Human cDNA encoding PRO20026.
XX
KW Human; ss; gene; interleukin 17; IL-17; IL17 receptor; angiogenesis;
KW T-lymphocyte proliferation; inflammatory cell infiltration;
KW immune related disorder; systemic lupus erythematosus; osteoarthritis;
KW rheumatoid arthritis; spondyloarthritis; systemic sclerosis;
KW Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia;
KW thyroiditis; diabetes mellitus; immune-mediated renal disease;
KW demyelinating disease; Guillain-Barre syndrome; hepatobiliary disease;
KW hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis;
KW allergic-mediated skin disease; erythema multiforme; contact dermatitis;
KW allergic disease; asthma; atopic dermatitis; food hypersensitivity;
KW urticaria; immunologic disease of the lung; eosinophilic pneumonia;
KW idiopathic pulmonary fibrosis; transplantation associated disease;
KW graft-versus-host disease.
XX
OS Homo sapiens.
XX
PN US2003003546-A1.
XX
PD 02-JAN-2003.
XX
PF 22-MAR-2001; 2001US-00816744.
XX
PR 15-MAY-1998; 98US-0085579P.
PR 23-DEC-1998; 98US-0113621P.
PR 08-MAR-1999; 99WO-US005028.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 14-MAY-1999; 99US-00311832.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 09-JUN-1999; 99US-0138387P.
PR 23-DEC-1999; 99US-0172096P.
PR 30-DEC-1999; 99WO-US031274.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000WO-US007532.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-JUN-2000; 2000US-0213807P.
PR 24-AUG-2000; 2000WO-US023328.
PR 26-OCT-2000; 2000US-0242837P.
PR 26-OCT-2000; 2000US-0244072P.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
XX
XX (GETH) GENENTECH INC.
XX
XX Chen J, Filvaroff E, Pong S, Goddard A, Godowski P, Grimaldi C;
PI Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;
PI Watanabe C, Williams PM, Wood WI, Yansura D;
XX

DR WPI: 2003-428843/40.
DR P-PSDB; ABU89705.
XX
PT New PRO polypeptides and polynucleotides homologous to interleukin-17,
PT useful for treating e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, or systemic
PT sclerosis.
XX
PS Claim 2; Fig 17; 129pp; English.
XX
CC The invention relates to a nucleic acid having similarity to interleukin-
CC 17 (IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence
CC identity to a nucleotide sequence which: (a) encodes a polypeptide having
CC a sequence of appearing as ABU89697-ABU89700 and ABU89702-ABU89705 (PI-
CC P8), lacking or having its associated signal peptide; (b) encodes an
CC extracellular domain of PI-P8 lacking its associated signal peptide; (c)
CC consists of a sequence of appearing as ACA89850-ACA89853 and ACA89855-
CC ACA89858687; or (d) consists of the full-length coding sequence of
CC selected from SI-S8, and of the cDNA deposited under ATCC accession
CC number 209866, 203552, PTA-1185, PTA-2108, PTA-202, PTA-1535, PTA-1082 or
CC PTA-2591. Also included are expression vectors, host cells, encoded
CC proteins, chimaeric proteins, antibodies, ant/agonists, compounds
CC inhibiting the expression of SI-S8 or activity (or mimicking the activity
CC of) of PI-P8, stimulating/inhibiting the proliferation of T-lymphocytes
CC using the polypeptides or ant/agonists, enhancing the infiltration of
CC inflammatory cells into a tissue of a mammal by administering a PRO1031
CC polypeptide, its an agonist or antagonist, and inhibiting angiogenesis
CC induced by a PRO1031 polypeptide or its agonist in a mammal by
CC administering a PRO1031 polypeptide, its ant/agonist or an anti-PRO1031
CC antibody. The proteins, antibodies, ant/agonists and compounds are useful
CC for treating an immune related disorder such as systemic lupus
CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC demyelinating disease of the central or peripheral nervous system,
CC chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes an IL17 or IL17
CC receptor homologue of the invention
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
Query Match 87.0%; Score 2074.2; DB 8; Length 2319;
Best Local Similarity 98.1%; Pred No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;
QY 252 AGGGAGTGGGGCCAGCCAGCGAAGAACAGTGGGCTGTACAAATCAATCAATGACA 311
DB 122 AGGGAGTGGGGCCAGCCAGCGAAGAACAGTGGGCTGTACAAATCAATGACA 181
QY 312 ATTGTACCACTTGTGAATCAGTGGGAGCATGTGCTGACGCCAGATATCA 371
DB 182 ATTGTACCACTTGTGAATCAGTGGGAGCATGTGCTGACGCCAGATATCA 241
QY 372 CCATCAGCCAGTATCTTGGCATGACCAAGTGGGAGTCAACATCTTTGGTCCCCAGGG 431
DB 242 CCATCAGCCAGTATGCTTGGCATGACCAAGTGGGAGTCAACATCTTTGGTCCCCAGGG 301
QY 432 CCTCGGCATCGAATTCCTGAAAGGATTCGGGTAATCTGGAGAGCTGAAGTCGGAGG 491
DB 302 CCTCGGCATCGAATTCCTGAAAGGATTCGGGTAATCTGGAGAGCTGAAGTCGGAGG 361

QY 492 GAAGACAGTCCCAACTGATTTCTAAAGGATCGAAGCAGCTCAACAGTAGCTTCAAAA 551
DB 362 GAAGACAGTCCCAACTGATTTCTAAAGGATCGAAGCAGCTCAACAGTAGCTTCAAAA 421
QY 552 GAACCTGGAATGGAATCTCAACCTTTCTGATATGAAATTTGAAACGGATTTATTCGTAA 611
DB 422 GAACCTGGAATGGAATCTCAACCTTTCTGATATGAAATTTGAAACGGATTTATTCGTAA 481
QY 612 AGGTGTCTCCCTTTCTCCATTAAGAAACGAAAGCAATTAACCCCTTCTCTTTAGAA 671
DB 482 AGGTGTCTCCCTTTCTCCATTAAGAAACGAAAGCAATTAACCCCTTCTCTTTAGAA 541
QY 672 CCCGAGCCTGTGACCTCTTTGTTACAGCCGGACAACTTAGCTTTGTAACCCCTTCTGGAAGC 731
DB 542 CCCGAGCCTGTGACCTCTTTGTTACAGCCGGACAACTTAGCTTTGTAACCCCTTCTGGAAGC 601
QY 732 CTGGAACCTGTGAACATCAGCA----- 753
DB 602 CTGGAACCTGTGAACATCAGCACTGGCTCGGACATGCGAGGTGCTCTTCGACCACGAC 661
QY 754 -GCATGGCTCGGACATGCGAGTGTCTTCGACCATGCGACGCAACTTGGCTTCGTT 812
DB 662 CGCATGGCTCGGACATGCGAGTGTCTTCGACCATGCGACGCAACTTGGCTTCGTT 721
QY 813 TCTTTCTATCTTCACTACAAGCTCAAGCAAGGACCTTTCAAGCGAAAGACCTGTGAAGC 872
DB 722 TCTTTCTATCTTCACTACAAGCTCAAGCAAGGACCTTTCAAGCGAAAGACCTGTGAAGC 781
QY 873 AGGAGCAAACTACAGAGACGACGCTGCTCTTCAAAATGTTTCTCGAGGGATTAATA 932
DB 782 AGGAGCAAACTACAGAGACGACGCTGCTCTTCAAAATGTTTCTCGAGGGATTAATA 841
QY 933 TAATTGAGCTGGTGGATGACATTAACACACAGAAAGTGAATGATTCCTTTAAAGC 992
DB 842 TAATTGAGCTGGTGGATGACATTAACACACAGAAAGTGAATGATTCCTTTAAAGC 901
QY 993 CAGTGCACTCCCGTGGCGCGGCCCATCAGAGCCGTGGCCCATCAGAGTGCCTGCTAG 1052
DB 902 CAGTGCACTCCCGTGGCGCGGCCCATCAGAGCCGTGGCCCATCAGAGTGCCTGCTAG 961
QY 1053 TCATATCGGATTCGCGACGCTCTTCACTGTGTGTGCGCGGCAAGCAACAGAAATA 1112
DB 962 TCATATCGGATTCGCGACGCTCTTCACTGTGTGTGCGCGGCAAGCAACAGAAATA 1021
QY 1113 TATATTCACATTTAGATGAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCA 1172
DB 1022 TATATTCACATTTAGATGAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCA 1081
QY 1173 GAGAGAGCTCCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1232
DB 1082 GAGAGAGCTCCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1141
QY 1233 ATCATGATGATGCTCGTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1292
DB 1142 ATCATGATGATGCTCGTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1201
QY 1293 TGGCTCTGGACCTGTGGAGAGCTTTCAGCTCTCTGAGAGAGGCGAGAGAAATGGGTCA 1352
DB 1202 TGGCTCTGGACCTGTGGAGAGCTTTCAGCTCTCTGAGAGAGGCGAGAGAAATGGGTCA 1261
QY 1353 TCCAGAGAGTCCAGAGTCCAGTGTTCATCATTTGTTGTTTCCAAAGGTATGAGTACT 1412
DB 1262 TCCAGAGAGTCCAGAGTCCAGTGTTCATCATTTGTTGTTTCCAAAGGTATGAGTACT 1321
QY 1413 TTGTGGAACAAGAACTTACAAAACAAGAGAGTGGCGGAGGCTCGGGGAAAGAGAGC 1472
DB 1322 TTGTGGAACAAGAACTTACAAAACAAGAGAGTGGCGGAGGCTCGGGGAAAGAGAGC 1381
QY 1473 TCTTCTGTGGCGGTGTGAGCAATTCGAAAGAGTCCGCGAGCCAGCAGAGTTCGT 1532
DB 1382 TCTTCTGTGGCGGTGTGAGCAATTCGAAAGAGTCCGCGAGCCAGCAGAGTTCGT 1441
QY 1533 CCGGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTTATTCCTGCGAGGAGAGCGTCC 1592

Db 1442 CGCGGCGCTCAGCAAGTTATTCGCGCTCTACTTTGATTATTCCTCGCAGGAGCGTCC 1501
Qy CGGATATCTAGACCTGAGTACCAAGTACAGACTCATGACAACTTCTCAGCTCTGTT 1652
Db CGGATATCTAGACCTGAGTACCAAGTACAGACTCATGACAACTTCTCAGCTCTGTT 1561
Qy CCCACTTCACCTCCGAGACCAAGCTCCAGGAGCGGGGAGCAGACACGCGGACAGGCA 1712
Db CCCACTTCACCTCCGAGACCAAGCTCCAGGAGCGGGGAGCAGACACGCGGACAGGCA 1621
Qy GCAGAAGAACTACTTCCGAGCAAGTACAGCGCGTCCCTATACGTCCCAATTTGCAACA 1772
Db GCAGAAGAACTACTTCCGAGCAAGTACAGCGCGTCCCTATACGTCCCAATTTGCAACA 1681
Qy TGACACAGTTATTCAGAGAGCGGAGTTCGTTGAAAGCAGTTCTGTTCCCTCCATC 1832
Db TGACACAGTTATTCAGAGAGCGGAGTTCGTTGAAAGCAGTTCTGTTCCCTCCATC 1741
Qy CTCCTCCACTGCGCTACCGGAGCGAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892
Db CTCCTCCACTGCGCTACCGGAGCGAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801
Qy ATGATGTATGTGCAAAACAGCGGCTGAGAGTACTTCTGCTAAAGTACAGGCGGCTG 1952
Db ATGATGTATGTGCAAAACAGCGGCTGAGAGTACTTCTGCTAAAGTACAGGCGGCTG 1861
Qy TTCTTGGGGCAACCGGACAGCGGCTGAGAGTACTTCTGCTAAAGTACAGGCGGCTG 2012
Db TTCTTGGGGCAACCGGACAGCGGCTGAGAGTACTTCTGCTAAAGTACAGGCGGCTG 1921
Qy AAGAGGGGAGCGCGGCTGCGCTTACGCTGAGCGCGGCTGCAACCCCTGCTGCACA 2072
Db AAGAGGGGAGCGCGGCTGCGCTTACGCTGAGCGCGGCTGCAACCCCTGCTGCACA 1981
Qy CGGTCAAAAGCGGCAAGCGGCTCGGACATGCGCGGAGCTCAGGCACTATGACTGCTG 2132
Db CGGTCAAAAGCGGCAAGCGGCTCGGACATGCGCGGAGCTCAGGCACTATGACTGCTG 2041
Qy TGCCCTCATCCAGCTGCTCTGCACTGATGGAAGAGTCTCGAGCGGACAGAGAGAA 2192
Db TGCCCTCATCCAGCTGCTCTGCACTGATGGAAGAGTCTCGAGCGGACAGAGAGAA 2101
Qy CGCTTCCTCAGCAGAGCGGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2252
Db CGCTTCCTCAGCAGAGCGGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2161
Qy CCCTTCCTTCCAGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2312
Db CCCTTCCTTCCAGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2221
Qy ACATGATGAATCCAGCGGCTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2372
Db ACATGATGAATCCAGCGGCTGCGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2281
Qy CACTTTA 2379
Db CACTTTA 2288

RESULT 11

ACM64642
ID ACM64642 standard; cDNA; 2319 BP.
XX
AC
ACA64642;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human cDNA encoding IL-17 family member, PRO200206.
XX
KW Human; ss; gene; interleukin-17; IL-17; cytokine; T-lymphocyte;
KW inflammatory cell; angiogenesis; gene therapy; immune-related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;

KW systemic sclerosis; idiopathic inflammatory myopathy; Sjogren's syndrome;
KW sarcoidosis; autoimmune hemolytic anaemia; thyroiditis; psoriasis;
KW diabetes mellitus; demyelinating disease; Guillain-Barre syndrome;
KW autoimmune chronic active hepatitis; primary biliary cirrhosis;
KW inflammatory bowel disease; immune-mediated skin disease;
KW contact dermatitis; allergic disease; asthma; urticaria;
KW eosinophilic pneumonia; idiopathic pulmonary fibrosis;
KW transplantation-associated disease; graft-versus-host disease.
OS
XX Homo sapiens.
XX US2003008815-A1.
XX 09-JAN-2003.
XX 20-DEC-2000; 2000US-00747259.
XX 14-MAY-1999; 99US-00311832.
XX 23-DEC-1999; 99US-0172096P.
XX 30-DEC-1999; 99WO-US031274.
XX 11-JAN-2000; 2000US-0175481P.
XX 18-FEB-2000; 2000WO-US004341.
XX 02-MAR-2000; 2000WO-US005841.
XX 21-MAR-2000; 2000US-0191007P.
XX 21-MAR-2000; 2000WO-US007532.
XX 02-JUN-2000; 2000WO-US015264.
XX 20-JUN-2000; 2000US-0213087P.
XX 22-AUG-2000; 2000US-0064848.
XX 24-AUG-2000; 2000WO-US023328.
XX 24-OCT-2000; 2000US-0242837P.
XX 10-NOV-2000; 2000WO-US030873.
XX 28-NOV-2000; 2000US-0253646P.
XX 01-DEC-2000; 2000WO-US032678.
XX (GETH) GENENTECH INC.
XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi C;
PI Gurney AL, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;
PI Watanabe C, Williams PM, Wood WI, Yansura DG;
XX WPI; 2003-341350/32.
DR P-PSDB; ABU72600.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1031,
PT PRO1122, PRO10272, useful in molecular biology, chromosome and gene
PT mapping, in generating antisense RNA and DNA, and in gene therapy.
XX Claim 2; Fig 17; 148pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 80%
XX sequence identity to 8 cDNA sequences encoding PRO polypeptides (or their
XX extracellular domains) which are members of the interleukin-17 (IL-17)
XX family of cytokines. Also included are expression vectors, host cells,
XX the PRO polypeptides, chimeric molecules comprising the above
XX polypeptides fused to a heterologous amino acid sequence, an anti-PRO
XX antibody, a composition comprising the above polypeptide (or its agonist
XX or antagonist, or the antibody cited above) in combination with a
XX carrier, determining the presence of a PRO polypeptide in a sample,
XX identifying a compound that mimics or inhibits the activity of the PRO
XX polypeptides cited above, or a compound that inhibits the expression of a
XX gene encoding the above polypeptides, stimulating or inhibiting the
XX proliferation of T-lymphocytes, enhancing or decreasing the infiltration
XX of inflammatory cells into a tissue of a mammal and inhibiting or
XX stimulating angiogenesis induced by a PRO1031 polypeptide or its agonist
XX in a mammal. The nucleic acid is useful in molecular biology, e.g. use as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA, and in gene therapy. The polynucleotide may also
XX be used in preparing PRO polypeptides by recombinant techniques, and in
XX generating either transgenic animals or knock-out animals which, in turn,
XX are useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptide or the antibody is used in preparing a
XX medicament for treating a condition responsive to the polypeptide or
XX antibody, and in various diagnostic assays. For immune-related disorders,

these may be systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin disease, bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, immunologic disease of the lung, eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, transplantation-associated disease, graft rejection or graft-versus-host disease. The composition is useful in treating the above-mentioned immune-related diseases in a mammal, or in increasing or inhibiting the proliferation of T-lymphocytes, or increasing or decreasing the infiltration of inflammatory cells into a tissue of a mammal. The present sequence encodes a PRO polypeptide of the invention

XX SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Query Match 87.0%; Score 2074.2; DB 8; Length 2319;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

| | | | |
|----|-----|---|-----|
| Qy | 252 | AGGGAGTGGGGCCAGCCAGCAGAGAACAGTGGGCTGTACAACATCACCTTCAAAATATGACA | 311 |
| Db | 122 | AGGGAGTGGGGCCAGCCAGCAGAACAGTGGGCTGTACAACATCACCTTCAAAATATGACA | 181 |
| Qy | 312 | ATTGTACCACTACTTGAATCAGTGGGGAAGCATGTGATGCTGACGCCCAGAAATATCA | 371 |
| Db | 182 | ATTGTACCACTACTTGAATCAGTGGGGAAGCATGTGATGCTGACGCCCAGAAATATCA | 241 |
| Qy | 372 | CCATCAGCAGTATGCTTGGCATGACCAAGTGGGAGTCAACCATCTTTGGTCCCCAGGG | 431 |
| Db | 242 | CCATCAGCAGTATGCTTGGCATGACCAAGTGGGAGTCAACCATCTTTGGTCCCCAGGG | 301 |
| Qy | 432 | CCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG | 491 |
| Db | 302 | CCCTCGGCATCGAATTCCTGAAAGATTTCCGGTAAATCTGGAGAGCTGAAGTCGGAGG | 361 |
| Qy | 492 | GAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA | 551 |
| Db | 362 | GAAGACAGTGCACCAACTGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA | 421 |
| Qy | 552 | GAACTGGAAATGGAATCTCAACTTTCTTGAATATGAATTTGAAACGGAATATTTCGTAA | 611 |
| Db | 422 | GAACTGGAAATGGAATCTCAACTTTCTTGAATATGAATTTGAAACGGAATATTTCGTAA | 481 |
| Qy | 612 | AGTTGTCCCTTTCTTCCATTAATAACGAAGCAATTACCACTTTCTTTCTTTAGAA | 671 |
| Db | 482 | AGTTGTCCCTTTCTTCCATTAATAACGAAGCAATTACCACTTTCTTTCTTTAGAA | 541 |
| Qy | 672 | CCCGAGCTGTGAACCTGTGTGTACAGCCGGACAATCTAGCTTGTAAACCCCTTCTGGAAGC | 731 |
| Db | 542 | CCCGAGCTGTGAACCTGTGTGTGTACAGCCGGACAATCTAGCTTGTAAACCCCTTCTGGAAGC | 601 |
| Qy | 732 | CTCGGAACCTGAAATCAGCCA----- | 753 |
| Db | 602 | CTCGGAACCTGAAATCAGCCAGCATGGCTCGGAATGGCTGGATGTCTTCGACCAACGCAAC | 661 |
| Qy | 754 | -GCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCAACCGCAAACTTCGGCTTCCGTT | 812 |
| Db | 662 | CGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGCAACCGCAAACTTCGGCTTCCGTT | 721 |
| Qy | 813 | TCTTCTATCTTCACTACAGCTCAAGCAAGGAGCCTTTCAAGCGAAAGACCTGTGAAGC | 872 |
| Db | 722 | TCTTCTATCTTCACTACAGCTCAAGCAAGGAGCCTTTCAAGCGAAAGACCTGTGAAGC | 781 |

| | | | |
|----|------|--|------|
| Qy | 873 | AGGAGCAAACTACAGAGACGAACAGCTGCCTCTCTTCAAAATGTTTCTCCAGGGGATTAATA | 932 |
| Db | 782 | AGGAGCAAACTACAGAGATGACAGCTGCCTCTCTTCAAAATGTTTCTCCAGGGGATTAATA | 841 |
| Qy | 933 | TAATTGAGCTGGTGGATGACACTAAACAACAAGAAAGATGATGATATATCCCTTAAGC | 992 |
| Db | 842 | TAATTGAGCTGGTGGATGACACTAAACAACAAGAAAGATGATGATATATCCCTTAAGC | 901 |
| Qy | 993 | CAGTGCACTCCCGTGGGCGCGCCCATCAGAGCCGTGGCCATCACAGTGCACCTGGTAG | 1052 |
| Db | 902 | CAGTGCACTCCCGTGGGCGCGCCCATCAGAGCCGTGGCCATCACAGTGCACCTGGTAG | 961 |
| Qy | 1053 | TCATATCGGATTCGCGACCGCTCTTCACTGTGTGTCGCCGAAGAACACAAGAAATA | 1112 |
| Db | 962 | TCATATCGGATTCGCGACCGCTCTTCACTGTGTGTCGCCGAAGAACACAAGAAATA | 1021 |
| Qy | 1113 | TATATTCACATTTAGATGAAGAGAGCTCTGAGCTTCCACATACACTGCAGCATCCCAA | 1172 |
| Db | 1022 | TATATTCACATTTAGATGAAGAGAGCTCTGAGCTTCCACATACACTGCAGCATCCCAA | 1081 |
| Qy | 1173 | GAGAGAGCTCCG | 1232 |
| Db | 1082 | GAGAGAGCTCCG | 1141 |
| Qy | 1233 | ATCATGAATGTGCTCCAGTGTTCGCCTACTTCTCCAGGACTTCTGTGGCTGTGAGG | 1292 |
| Db | 1142 | ATCATGAATGTGCTCCAGTGTTCGCCTACTTCTCCAGGACTTCTGTGGCTGTGAGG | 1201 |
| Qy | 1293 | TGGCTCTGGAGCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGCGCAGAGAAATGGGTCA | 1352 |
| Db | 1202 | TGGCTCTGGAGCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGCGCAGAGAAATGGGTCA | 1261 |
| Qy | 1353 | TCCAGAGAGTCCAGAGTCCAGTTCATCTGTTGGTGTTCCTCAAAAGGTATGAAGTACT | 1412 |
| Db | 1262 | TCCAGAGAGTCCAGAGTCCAGTTCATCTGTTGGTGTTCCTCAAAAGGTATGAAGTACT | 1321 |
| Qy | 1413 | TTGTGGCAAGAGAACTACAAACAACAAGAGAGTGGCCGAGGCTCCGGGGAAGAGAGC | 1472 |
| Db | 1322 | TTGTGGCAAGAGAACTACAAACAACAAGAGAGTGGCCGAGGCTCCGGGGAAGAGAGC | 1381 |
| Qy | 1473 | TCCTTCTGGTGGCGGTGTGAGCCATTCGCGAAGAGCTCCGCGCAGGCCACAGCAGATTCGT | 1532 |
| Db | 1382 | TCCTTCTGGTGGCGGTGTGAGCCATTCGCGAAGAGCTCCGCGCAGGCCACAGCAGATTCGT | 1441 |
| Qy | 1533 | CCGCGGCGCTCAGCAAGTTCGCGCTCTACTTTGATTTCTCTCGAGGAGCAGCTGCC | 1592 |
| Db | 1442 | CCGCGGCGCTCAGCAAGTTCGCGCTCTACTTTGATTTCTCTCGAGGAGCAGCTGCC | 1501 |
| Qy | 1593 | CCGCTATCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTT | 1652 |
| Db | 1502 | CCGCTATCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTT | 1561 |
| Qy | 1653 | CCCACTTGCACTCCGAGACCAAGGCTCAGAGAGCGCGGCGCAGCACHCGCAGAGGCA | 1712 |
| Db | 1562 | CCCACTTGCACTCCGAGACCAAGGCTCAGAGAGCGCGGCGCAGCACHCGCAGAGGCA | 1621 |
| Qy | 1713 | GCAGAAGCAACTCTTCGAGAGCAAGTTCAGCGCGCTCCCTATACGTGCCATTTGCAACA | 1772 |
| Db | 1622 | GCAGAAGCAACTCTTCGAGAGCAAGTTCAGCGCGCTCCCTATACGTGCCATTTGCAACA | 1681 |
| Qy | 1773 | TGCAACCACTTTATTCAGAGAGAGCCGAGCTGGTTTCGAAAGAGAGTTCCTTCCCTTCATC | 1832 |
| Db | 1682 | TGCAACCACTTTATTCAGAGAGAGCCGAGCTGGTTTCGAAAGAGAGTTCCTTCCCTTCATC | 1741 |
| Qy | 1833 | CTCTTCACTCGGCTACCGGAGCAGCTTTGGAGAAATTTTGATTCGGGCTTGGTTTTAA | 1892 |
| Db | 1742 | CTCTTCACTCGGCTACCGGAGCAGCTTTGGAGAAATTTTGATTCGGGCTTGGTTTTAA | 1801 |
| Qy | 1893 | ATGATGTCATCTGCAAAACAGGGCTGAGAGTGAATCTCTGCTTAAAGGTAGAGCGCGCTG | 1952 |
| Db | 1802 | ATGATGTCATCTGCAAAACAGGGCTGAGAGTGAATCTCTGCTTAAAGGTAGAGCGCGCTG | 1861 |
| Qy | 1953 | TTTCTGGGGCAACCGGACCGAGCTCCAGCAGAGAGTTCAGCATGGGGGCGCTTGGACC | 2012 |

Db 1862 TTCTTGGGCAACCGGACGAGCCGACTCCAGCAGCAGAGTCAGCATGGGGCCTGGACC 1921
Qy 2013 AAGACGGGGAGCCCGGCTGCTTGAAGTGGCGCCCTGCAACCCCTGCTGCACA 2072
Db 1922 AAGACGGGGAGCCCGGCTGCTTGAAGTGGCGCCCTGCAACCCCTGCTGCACA 1981
Qy 2073 CGGTGAAGCCGGCAGCCCTCGGACATGCCGCGGACTCAGGCATCTATGACTCGTCTG 2132
Db 1982 CGGTGAAGCCGGCAGCCCTCGGACATGCCGCGGACTCAGGCATCTATGACTCGTCTG 2041
Qy 2133 TGCCCTCATCCGAGTGTCTTGCACATGATGGAAGGACTCTCGACGACGACAGAGAAA 2192
Db 2042 TGCCCTCATCCGAGTGTCTTGCACATGATGGAAGGACTCTCGACGACGACAGAGAAA 2101
Qy 2193 CGTCTTCCCTGACGAGAGCGTGTCTCTTCAAGGCTGGTGAGGAGAACTCTCTG 2252
Db 2102 CGTCTTCCCTGACGAGAGCGTGTCTCTTCAAGGCTGGTGAGGAGAACTCTCTG 2161
Qy 2253 CCCTTCCCTTCAAGCTCTCTTCTGGGTATGCAAAAGCAGATCTTGGTTGCCGCGAGCT 2312
Db 2162 CCCTTCCCTTCAAGCTCTCTTCTGGGTATGCAAAAGCAGATCTTGGTTGCCGCGAGCT 2221
Qy 2313 ACATGATGAATCCACGCGTGCCTTGTGTAACAAAGAGAGTCTTAAGCATTGC 2372
Db 2222 ACATGATGAATCCACGCGTGCCTTGTGTAACAAAGAGAGTCTTAAGCATTGC 2281
Qy 2373 CACTTTA 2379
Db 2282 CACTTTA 2288

RESULT 12

AD43240
ID ADA43240 standard; cDNA; 2319 BP.

XX AC ADA43240;

XX DT 20-NOV-2003 (first entry)

XX DE Human interleukin 17 related mammalian cytokine polypeptide cDNA #9.

XX KW ss; Gene; interleukin 17; cytokine; IL-17E; immune-related disease;
KW inflammatory disease; psoriasis; asthma; allergic rhinitis;
KW rheumatoid arthritis; human; interleukin 17 related mammalian cytokine.

XX OS Homo sapiens.

XX PN US6579520-B2.

XX PD 17-JUN-2003.

XX PF 22-MAR-2001; 2001US-00816744.

XX PR 15-MAY-1998; 98US-0085579P.

XX PR 23-DEC-1998; 98US-0113621P.

XX PR 21-APR-1999; 99US-0130232P.

XX PR 26-APR-1999; 99US-0131022P.

XX PR 14-MAY-1999; 99US-00311832.

XX PR 14-MAY-1999; 99US-0134287P.

XX PR 09-JUN-1999; 99US-0138387P.

XX PR 23-DEC-1999; 99US-0172096P.

XX PR 11-JAN-2000; 2000US-0175481P.

XX PR 21-MAR-2000; 2000US-0191007P.

XX PR 22-JUN-2000; 2000US-0213807P.

XX PR 24-OCT-2000; 2000US-0242837P.

XX PR 26-OCT-2000; 2000US-0244072P.

XX PR 28-NOV-2000; 2000US-0253646P.

XX (GETH) GENENTECH INC.

XX PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski P, Grimaldi C;

PI Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandlen R;

PI Watanabe C, Williams PM, Wood WI, Yansura D;
XX WPI; 2003-615512/58.
DR P-PSDB; ADA43241.
XX
PT New interleukin 17 related mammalian cytokine polypeptide (IL-17E)
PT polypeptide, useful for preparing composition for treating immune-related
PT or inflammatory diseases, e.g. psoriasis, asthma, allergic rhinitis or
PT rheumatoid arthritis.
XX
XX Example 8; Fig 17; 235pp; English.
PS
CC The invention relates to a new isolated interleukin 17 related mammalian
CC cytokine polypeptide (IL-17E). The polypeptide is useful for preparing a
CC composition for treating immune-related or inflammatory diseases, e.g.
CC psoriasis, asthma, allergic rhinitis or rheumatoid arthritis. The present
CC sequence represents cDNA encoding a human interleukin 17 related
CC mammalian cytokine polypeptide.
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;

Query Match 87.0%; Score 2074.2; DB 9; Length 2319;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

Qy 252 AGGGAGTGGGCGCAGCAGCAAGTGGCTGTACAACATCACTTCAAAATATGACA 311

Db 122 AGGGAGTGGGCGCAGCAGCAAGTGGCTGTACAACATCACTTCAAAATATGACA 181

Qy 312 ATTGTACACCTACTTGAATTCAGTGGGAAGCATGTGATGCTGACGCCCAGATATCA 371

Db 182 ATTGTACACCTACTTGAATTCAGTGGGAAGCATGTGATGCTGACGCCCAGATATCA 241

Qy 372 CCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATCTTCTGGTCCCAGGG 431

Db 242 CCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATCTTCTGGTCCCAGGG 301

Qy 432 CCCTCGGCATCGAATTCCTGAAAGGATTCGGGTAATACTGGAGGAGCTGAAGTCGGAGG 491

Db 302 CCCTCGGCATCGAATTCCTGAAAGGATTCGGGTAATACTGGAGGAGCTGAAGTCGGAGG 361

Qy 492 GAAGACAGTGCACCAACTGATTCCTAAAGGATCGGAGCAGCTCAAGTAGCTTCAAAA 551

Db 362 GAAGACAGTGCACCAACTGATTCCTAAAGGATCGGAGCAGCTCAAGTAGCTTCAAAA 421

Qy 552 GAACTGGAATCGAATCTCAACCTTCTCTGAATATGAAATTTGAAACGATTTATTCGTAA 611

Db 422 GAACTGGAATCGAATCTCAACCTTCTCTGAATATGAAATTTGAAACGATTTATTCGTAA 481

Qy 612 AGGTTGTCCCTTTTCTTCCATTAATAAAGCAATTAACACCTTCTTCTTTAGAA 671

Db 482 AGGTTGTCCCTTTTCTTCCATTAATAAAGCAATTAACACCTTCTTCTTTAGAA 541

Qy 672 CCCGAGCCTGTGACCTGTGTGTATAGCCGGAATCTAGCTTGTAAACCTTCTGGAAGC 731

Db 542 CCCGAGCCTGTGACCTGTGTGTATAGCCGGAATCTAGCTTGTAAACCTTCTGGAAGC 601

Qy 732 CTGCGAAGCTGAACATCAGCCA----- 753

Db 602 CTGCGAAGCTGAACATCAGCCA----- 661

Qy 754 -GCATGGCTCGGACATGCAAGTGTCTTCGACCATGACCGCAAACTTCGCTTCCGTT 812

Db 662 CGCATGGCTCGGACATGCAAGTGTCTTCGACCATGACCGCAAACTTCGCTTCCGTT 721

Qy 813 TCTTCTATCTTCACTAAGCTCAAGCAGGAGCCTTTCAAGGAAAGACCTGTAAGC 872

Db 722 TCTTCTATCTTCACTAAGCTCAAGCAGGAGCCTTTCAAGGAAAGACCTGTAAGC 781

Qy 873 AGGACCAACTACAGAGACGACCGCTCCCTTCAAAATGTTTCTCCAGGGGATTATA 932

Db 782 AGGACCAAACTACAGAGATGACCGCTCCCTTCAAAATGTTTCTCCAGGGGATTATA 841

| | | | | | | | |
|----|------|---|------|-----------|---|---|------|
| QY | 933 | TAATTGAGCTGGTGGATGACACTAACACAAAGAAAGTGTGATTTATGCTTAAAGC | 992 | Db | 1922 | AAGACGGGAGGCCCGCCCTTGACGGTAGCGCCCTGCAACCCCTGCTGCACA | 1981 |
| Db | 842 | TAATTGAGCTGGTGGATGACACTAACACAAAGAAAGTGTGATTTATGCTTAAAGC | 901 | QY | 2073 | CGGTAAAGCGGAGAGCCCTCGACATGCGCGGGGACTCAGGCATCTATGACTCGTCTG | 2132 |
| QY | 993 | CAGTGCACTCCCGGTGGGCGGCGCCATCAGAGCGGTGGCCCATCAGCTGCCACTGGTAG | 1052 | Db | 1982 | CGGTAAAGCGGAGAGCCCTCGACATGCGCGGGGACTCAGGCATCTATGACTCGTCTG | 2041 |
| Db | 902 | CAGTGCACTCCCGGTGGGCGGCGCCATCAGAGCGGTGGCCCATCAGCTGCCACTGGTAG | 961 | QY | 2133 | TGCCCTCATCCGAGCTGCTCTGCACTGATGGAAGGACTCTCGACGGACACAGAGAA | 2192 |
| QY | 1053 | TCATATCGGCAATTCGGCAGCGCTCTTCACTGTGATGTGCGGACAGAGCAACAGAAATA | 1112 | Db | 2042 | TGCCCTCATCCGAGCTGCTCTGCACTGATGGAAGGACTCTCGACGGACACAGAGAA | 2101 |
| Db | 962 | TCATATCGGCAATTCGGCAGCGCTCTTCACTGTGATGTGCGGACAGAGCAACAGAAATA | 1021 | QY | 2193 | CGTCTTCCCTGACGAGAGAGGTGTCTCTCTTTCAGGCTTGGGTGAGGAGAACTCTCTG | 2252 |
| QY | 1113 | TATATTACATTTAGATCAAGAGAGCTCTGAGTCTTCCACATACACTCCAGCACTCCCAA | 1172 | Db | 2102 | CGTCTTCCCTGACGAGAGAGGTGTCTCTCTTTCAGGCTTGGGTGAGGAGAACTCTCTG | 2161 |
| Db | 1022 | TATATTACATTTAGATCAAGAGAGCTCTGAGTCTTCCACATACACTCCAGCACTCCCAA | 1081 | QY | 2253 | CCCTTCTTCCCAAGCTCCTCTCTTCTGGGTGATGCAAGAGAGATCTTGGTTGCCGAGCT | 2312 |
| QY | 1173 | GAGAGAGCTCCGGCGGCGGCGAAGGTCTTTCTCTGCTATTTCAGTAAAGATGGCCAGA | 1232 | Db | 2162 | CCCTTCTTCCCAAGCTCCTCTCTTCTGGGTGATGCAAGAGAGATCTTGGTTGCCGAGCT | 2221 |
| Db | 1082 | GAGAGAGCTCCGGCGGCGGCGAAGGTCTTTCTCTGCTATTTCAGTAAAGATGGCCAGA | 1141 | QY | 2313 | ACACTGATGAACTCCACGCGTCCGCCCTTTGTAAACAAAGAGTCTTAAGCATTTGC | 2372 |
| QY | 1233 | ATCATGAATGTGCTCAGTGTGTTTGGCTTACTTCTCCAGACTTCTGTGGCTGTGAGG | 1292 | Db | 2222 | ACACTGATGAACTCCACGCGTCCGCCCTTTGTAAACAAAGAGTCTTAAGCATTTGC | 2281 |
| Db | 1142 | ATCATGAATGTGCTCAGTGTGTTTGGCTTACTTCTCCAGACTTCTGTGGCTGTGAGG | 1201 | QY | 2373 | CACTTTA 2379 | |
| QY | 1293 | TGGCTCTGCACTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAAATGGGTCA | 1352 | Db | 2282 | CACTTTA 2288 | |
| Db | 1202 | TGGCTCTGCACTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAAATGGGTCA | 1261 | RESULT 13 | | | |
| QY | 1353 | TCCAGAGATCCACGAGTCCAGTTCATCATTTGTGTTTGTTCAGTAAAGTATGAAGTACT | 1412 | ADA49781 | | | |
| Db | 1262 | TCCAGAGATCCACGAGTCCAGTTCATCATTTGTGTTTGTTCAGTAAAGTATGAAGTACT | 1321 | ID | ADA49781 | standard; cdna; 2319 BP. | |
| QY | 1413 | TTGTGGACAGAGAACTACAAAACAAAAGAGGTGGCCGAGGCTCGGGGAAAGAGAGC | 1472 | XX | ADA49781; | | |
| Db | 1322 | TTGTGGACAGAGAACTACAAAACAAAAGAGGTGGCCGAGGCTCGGGGAAAGAGAGC | 1381 | XX | 20-NOV-2003 (first entry) | | |
| QY | 1473 | TCCTTCTGGTGGCGGTGTCAGCATTGCGGAAAGCTCCGCCAGGCCAAGCAGAGTTTGGT | 1532 | XX | Human interleukin-17/interleukin-17 receptor related PRO20026 cdna. | | |
| Db | 1382 | TCCTTCTGGTGGCGGTGTCAGCATTGCGGAAAGCTCCGCCAGGCCAAGCAGAGTTTGGT | 1441 | XX | Human; interleukin-17; IL-17; gene; ss; dermatological; | | |
| QY | 1533 | CCGGCGGCTCAGCAAGTTTATCGCGCTCTACTTTTGAATTTCTTCTCGAGGAGACGTCC | 1592 | KW | immunosuppressive; antinflammatory; antirheumatic; antiarthritic; | | |
| Db | 1442 | CCGGCGGCTCAGCAAGTTTATCGCGCTCTACTTTTGAATTTCTTCTCGAGGAGACGTCC | 1501 | KW | osteopathic; antianaemic; antidiabetic; antithyroid; haemostatic; | | |
| QY | 1593 | CCGTATCTAGACTGATGATACAAATGACAGCTCATGACAAATCTTCTCAGCTCTGTT | 1652 | KW | hepatotropic; antianaemic; antidiabetic; antithyroid; haemostatic; | | |
| Db | 1502 | CCGTATCTAGACTGATGATACAAATGACAGCTCATGACAAATCTTCTCAGCTCTGTT | 1561 | KW | gene therapy; immune related disorder; systemic lupus erythematosus; | | |
| QY | 1653 | CCCCTTGCCTCCGAGACCAAGCCCTCCAGGAGCCGGGCGAGCACACGCGACAGGGCA | 1712 | KW | rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; | | |
| Db | 1562 | CCCCTTGCCTCCGAGACCAAGCCCTCCAGGAGCCGGGCGAGCACACGCGACAGGGCA | 1621 | KW | spondyloarthropathy; systemic sclerosis; | | |
| QY | 1713 | GCAGAAAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTATACCTGCCATTTTGCACA | 1772 | KW | idiopathic inflammatory myopathy; Sjogren's syndrome; | | |
| Db | 1622 | GCAGAAAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTATACCTGCCATTTTGCACA | 1681 | KW | systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; | | |
| QY | 1773 | TGCACAGTTTATGACAGAGAGCCGACTGTGTTGAAAAGCAGTTCTTCTTCCATC | 1832 | KW | autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; | | |
| Db | 1682 | TGCACAGTTTATGACAGAGAGCCGACTGTGTTGAAAAGCAGTTCTTCTTCCATC | 1741 | KW | immune-mediated renal disease; demyelinating disease; | | |
| QY | 1833 | CTCCTCCACTGGCTTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA | 1892 | XX | Guillain-Barre syndrome; | | |
| Db | 1742 | CTCCTCCACTGGCTTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA | 1801 | XX | chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease; | | |
| QY | 1893 | ATGATGTATGTGCAAAACAGGGCTGAGAGTGAATTTCTGCTTAAAGGTAGAGCGGCTG | 1952 | XX | hepatitis; primary biliary cirrhosis; sclerosing cholangitis; | | |
| Db | 1802 | ATGATGTATGTGCAAAACAGGGCTGAGAGTGAATTTCTGCTTAAAGGTAGAGCGGCTG | 1861 | FT | inflammatory bowel disease; gluten-sensitive enteropathy; | | |
| QY | 1953 | TTCTTTGGGCAACCGGACAGCCGACTCCAGCAAGAGTCAAGTGGGGCTTGAGAC | 2012 | FT | Whipple's disease; skin disease; erythema multiforme; contact dermatitis; | | |
| Db | 1862 | TTCTTTGGGCAACCGGACAGCCGACTCCAGCAAGAGTCAAGTGGGGCTTGAGAC | 1921 | FT | psoriasis; allergic disease; asthma; allergic rhinitis; | | |
| QY | 2013 | AAGACGGGAGGCCCGCCCTTGACGGTAGCGCCCTGCAACCCCTGCTGCACA | 2072 | FT | apoc dermatitis; food hypersensitivity; urticaria; | | |
| | | | | XX | eosinophilic pneumonia; idiopathic pulmonary fibrosis; | | |
| | | | | XX | hypersensitivity pneumonitis; transplantation; graft rejection; | | |
| | | | | XX | graft-versus-host-disease. | | |
| | | | | XX | Homo sapiens. | | |
| | | | | XX | OS | | |
| | | | | XX | Key | Location/Qualifiers | |
| | | | | FT | CDS | 70..2256 | |
| | | | | FT | | /*tag= a | |
| | | | | FT | | /product= "PRO20026" | |
| | | | | FT | | /note= "Interleukin-17 and interleukin-17 receptor | |
| | | | | XX | | related protein" | |
| | | | | XX | US2002177188-A1. | | |
| | | | | XX | 28-NOV-2002. | | |
| | | | | XX | | | |

PF 05-JUN-2001; 2001US-00874503.
XX 15-MAY-1998; 98US-0085579P.
PR 23-DEC-1998; 98US-0113621P.
PR 08-MAR-1999; 99WO-US005028.
PR 21-APR-1999; 99US-0130232P.
PR 26-APR-1999; 99US-0131022P.
PR 14-MAY-1999; 99US-0134287P.
PR 14-MAY-1999; 99WO-US010733.
PR 09-JUN-1999; 99US-0138387P.
PR 23-DEC-1999; 99US-0172096P.
PR 30-DEC-1999; 99WO-US031274.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000WO-US007532.
PR 02-JUN-2000; 2000WO-US015264.
PR 22-JUN-2000; 2000US-0213807P.
PR 24-AUG-2000; 2000WO-US023328.
PR 24-OCT-2000; 2000US-0242837P.
PR 26-OCT-2000; 2000US-0244072P.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
XX (GETH) GENENTECH INC.
XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi JC;
PI Gurney A, Li H, Hillan K, Hymowitz SG, Tumas D, Starovozanik MA;
PI Lookeren WV, Vandlen R, Watanabe C, Williams PM, Wood WI;
PI Yansura DG;
XX WPI: 2003-605676/57.
DR P-PSDB; ADA49782.
XX Novel polypeptides having sequence similarity to interleukin-17 and
PT interleukin-17 receptor protein useful for treating, diagnosing immune
PT related disorders and treating degenerative cartilaginous disorder in a
PT mammal.
XX Claim 130; Fig 17; 140pp; English.
XX The invention describes an isolated polypeptide (I) having at least 80%
CC amino acid sequence identity to interleukin(IL)-17 and IL-17 receptor
CC protein. The novel PRO polypeptides are useful for treating an immune
CC related disorder such as systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis,
CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis,
CC diabetes mellitus, immune-mediated renal disease, demyelinating disease
CC of the central or peripheral nervous system, idiopathic demyelinating
CC polynuropathy, Guillain-Barre syndrome, chronic inflammatory
CC demyelinating polynuropathy, hepatobiliary disease, infectious or
CC autoimmune chronic active hepatitis, primary biliary cirrhosis,
CC granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel
CC disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or
CC immune-mediated skin disease, bullous skin disease, erythema multiforme,
CC contact dermatitis, psoriasis, allergic disease, asthma, allergic
CC rhinitis, atopic dermatitis, food hypersensitivity, urticaria,
CC immunologic disease of the lung, eosinophilic pneumonia, idiopathic
CC pulmonary fibrosis, hypersensitivity pneumonitis, transplantation
CC associated disease or graft rejection or graft-versus-host-disease, in a
CC mammal. An anti-(I)-antibody is useful for determining the presence of
CC PRO polypeptide in a sample suspected of containing the polypeptide and
CC for diagnosing an immune related disease in a mammal. (I) is useful for
CC identifying a compound that inhibits the activity of PRO polypeptide or
CC expression of gene encoding PRO polypeptide, by contacting cells which
CC normally express the polypeptide with a candidate compound, and

CC determining the lack of responsiveness by the cell or expression of the
CC gene. This sequence encodes a novel PRO polypeptide with sequence
CC similarity to interleukin-17 and the interleukin-17 receptor.
XX
XX Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
Query Match 87.0%; Score 2074.2; DB 9; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;
QY 252 AGGAGTGGGCGCCAGCAGCAAGAAACAGTGGGCTGTACAAATCACCTTCAAAATATGACA 311
DB 122 AGGAGTGGGCGCCAGCAGCAAGAAACAGTGGGCTGTACAAATCACCTTCAAAATATGACA 181
QY 312 ATTGTACCCACTTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAAATATCA 371
DB 182 ATTGTACCCACTTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCCAGAAATATCA 241
QY 372 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCACTTCTTTGGTCCCAGGGG 431
DB 242 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCACTTCTTTGGTCCCAGGGG 301
QY 432 CCCTGGCATCGAATTCCTGAAAGGATTTCCGGGTAATACTGAGGAGCTGAAGTCGGAGG 491
DB 302 CCCTGGCATCGAATTCCTGAAAGGATTTCCGGGTAATACTGAGGAGCTGAAGTCGGAGG 361
QY 492 GAAGACAGTGCACCAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551
DB 362 GAAGACAGTGCACCAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 421
QY 552 GAACCTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGATATTTTCGTAA 611
DB 422 GAACCTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGATATTTTCGTAA 481
QY 612 AGTTTGTCCCTTTCTTCCATTAAGAAAGCAAGCAATTAACACCTTCTTCTTTAGAA 671
DB 482 AGTTTGTCCCTTTCTTCCATTAAGAAAGCAAGCAATTAACACCTTCTTCTTTAGAA 541
QY 672 CCGGAGCTGTGACCTGTGTTTACAGCGGCAATCTAGCTTTGTAACCTTTCTGGAAGC 731
DB 542 CCGGAGCTGTGACCTGTGTTTACAGCGGCAATCTAGCTTTGTAACCTTTCTGGAAGC 601
QY 732 CTCGGAACCTCGAACATCAGCCA ----- 753
DB 602 CTCGGAACCTCGAACATCAGCCAAGCATGCGCATGCGGTGCTTTTCGACCAAGCAC 661
QY 754 -GCATGGCTCGGACATGACAGTGTCTTCGACCATGACCGCACAACTTCGGCTTCGGTT 812
DB 662 CGCATGGCTCGGACATGACAGTGTCTTCGACCATGACCGCACAACTTCGGCTTCGGTT 721
QY 813 TCTTCTATCTTCACTACAGCTCAAGCTCAAGCAGGAGACCTTTCAAGCGAAAGACCTGTAAGC 872
DB 722 TCTTCTATCTTCACTACAGCTCAAGCTCAAGCAGGAGACCTTTCAAGCGAAAGACCTGTAAGC 781
QY 873 AGGCAAACTACAGAGACGACCTGCTCTTCAAAATGTTTCTCCAGGGGATATA 932
DB 782 AGGCAAACTACAGAGATGACCTGCTCTTCAAAATGTTTCTCCAGGGGATATA 841
QY 933 TAAATTGAGCTGGTGAATGACATAACACAAAGAAAGTGTATGATATGCTTAAAGC 992
DB 842 TAAATTGAGCTGGTGAATGACATAACACAAAGAAAGTGTATGATATGCTTAAAGC 901
QY 993 CAGTGCACCTCCCGTGGGCGGCGCCATCAGAGCGCTGCGCCATCAGTGCACCTGGTAG 1052
DB 902 CAGTGCACCTCCCGTGGGCGGCGCCATCAGAGCGCTGCGCCATCAGTGCACCTGGTAG 961
QY 1053 TCATATCGGCATTTCGCGACGCTTCTTCACTGTGATGTGCGGCAAGCAACAAAGAAATA 1112
DB 962 TCATATCGGCATTTCGCGACGCTTCTTCACTGTGATGTGCGGCAAGCAACAAAGAAATA 1021
QY 1113 TATATTCAATTAGATGAAGAGAGCTGTGAGTCTTCCATACATACACTGCAGCACTCCCAA 1172
DB 1022 TATATTCAATTAGATGAAGAGAGCTGTGAGTCTTCCATACATACACTGCAGCACTCCCAA 1081

PT sclerosis.
XX Claim 2; Fig 17; 154pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequence encoding them. The novel
CC PRO polypeptides show sequence similarity to interleukin-17 (IL-17) and
CC to the IL-17 receptor. The PRO polypeptides, agonists, antagonists and
CC antibodies that specifically bind to the PRO polypeptides are useful for
CC treating an immune related disorder in a mammal, such as systemic lupus
CC erythematosus (SLE), rheumatoid arthritis, osteoarthritis, juvenile
CC chronic arthritis, spondyloarthritis, systemic sclerosis, idiopathic
CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC sarcoidosis, autoimmune hemolytic anaemia, diabetes mellitus, immune-
CC mediated renal disease, demyelinating disease of the central or
CC peripheral nervous system, Guillain-Barre syndrome, hepatobiliary
CC disease, immune-mediated skin disease, food hypersensitivity, urticaria,
CC or graft-versus-host disease. A composition comprising a PRO polypeptide,
CC agonist, antagonist or antibody is useful for the treatment of an immune
CC related disease in a mammal and is capable of increasing or inhibiting
CC the proliferation of T-lymphocytes in, or increasing or decreasing
CC infiltration of inflammatory cells into a tissue. The present sequence
CC encodes a human PRO polypeptide of the invention.
XX
SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
Query Match 87.0%; Score 2074.2; DB 10; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;
QY 252 AGGGAGTGGGGCCAGCCAGCAAGACAGTGGGCTGTACAAATCAATCAATATGACA 311
DB 122 AGGGAGTGGGGCCAGCCAGCAAGACAGTGGGCTGTACAAATCAATCAATATGACA 181
QY 312 ATTTGACCACTTCTGAATCCAGTGGGAAGCATGTGATGCTGACGCCCAAGATATCA 371
DB 182 ATTTGACCACTTCTGAATCCAGTGGGAAGCATGTGATGCTGACGCCCAAGATATCA 241
QY 372 CCATAGCCAGTATGTTGCCATGACCAAGTGGCAGTCAACATCTTTGGTCCCCAGGG 431
DB 242 CCATAGCCAGTATGTTGCCATGACCAAGTGGCAGTCAACATCTTTGGTCCCCAGGG 301
QY 432 CCTCGGCATGAAATCTCTGAAAGGATTTCCGGTAAATCTGAGGAGCTGAAAGTCCGAGG 491
DB 302 CCTCGGCATGAAATCTCTGAAAGGATTTCCGGTAAATCTGAGGAGCTGAAAGTCCGAGG 361
QY 492 GAAGACAGTCCCAACACTGATTTAAAGGATCCGAAGCAGCTCAACAGTACTTCAAAA 551
DB 362 GAAGACAGTCCCAACACTGATTTAAAGGATCCGAAGCAGCTCAACAGTACTTCAAAA 421
QY 552 GAACTGGAAATGAAATCTCAACCTTCTCGAATATGAAATTTGAAACGGATATTTCTGTA 611
DB 422 GAACTGGAAATGAAATCTCAACCTTCTCGAATATGAAATTTGAAACGGATATTTCTGTA 481
QY 612 AGTTGTCCTTTCTTCCATTAATAAGCAATTAACACCTTTCTTTTAGAA 671
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QY 672 CCGGAGCTGTGACCTGTTGTACAGCCGGAATCTAGCTTTGTAACCTTTCTGGAAGC 731
DB 542 CCGGAGCTGTGACCTGTTGTACAGCCGGAATCTAGCTTTGTAACCTTTCTGGAAGC 601
QY 732 CTCCGAACTGAAATCAATCAACCA----- 753
DB 602 CTCCGAACTGAAATCAATCAACCA----- 661
QY 754 -GCATGGCTCGACATGAGTGTCTTCCGACCATGCGACACTTTCGGCTTCGGTT 812
DB 662 CGCATGGCTCGGACATGAGTGTCTTCCGACCATGCGACACTTTCGGCTTCGGTT 721
QY 813 TCTTCTATCTTCACTACAAAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACCTGTAAGC 872
DB 722 TCTTCTATCTTCACTACAAAGCTCAAGCAGCAAGGACCTTTCAAGCGAAAGACCTGTAAGC 781

QY 873 AGGAGCAAACTACAGAGACGACAGCTGCTCCTTCAAAATGTTTCTCCAGGGGATTATA 932
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QY 933 TAAATGAGCTGGTGGATGACACTAAACAAGAAAGTATGATCATTTATGCTTTAAAGC 992
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QY 993 CAGTGCACTCCCCCTGGGCGCGGCATCAGAGCGCTGGCCATCAGTGGCACTGGTAG 1052
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QY 1353 TCCAGAGACTCCAGAGTCCAGTTCATCATTTGTGTTTGTTCCTCAAGTATGAAGTACT 1412
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QY 1833 CTCCTCCATGCGCTACCGGAGCGAGTCTTCGAGAAATTTGATTCGGGCTTGGTTTTAA 1892
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QY 1893 ATGATGTCATGTGCAAAACGAGGGCTGAGAGTGAATTCGCTCAAGGTAGAGGGCGGCTG 1952
DB 1802 ATGATGTCATGTGCAAAACGAGGGCTGAGAGTGAATTCGCTCAAGGTAGAGGGCGGCTG 1861

| | | | |
|----|------|--|------|
| Qy | 1953 | TTCTTGGGCAACCGGACAGCGACTCCAGCAGCAGAGTCAAGATGGGGGCTGGACC | 2012 |
| Db | 1862 | TTCTTGGGGCAACCGGACAGCGACTCCAGCAGCAGAGTCAAGATGGGGGCTGGACC | 1921 |
| Qy | 2013 | AAGACGGGGAGCGCGGCTGCGCTTGACGGTAGCGCGCCCTGCAACCCCTGCTGCACA | 2072 |
| Db | 1922 | AAGACGGGGAGCGCGGCTGCGCTTGACGGTAGCGCGCCCTGCAACCCCTGCTGCACA | 1981 |
| Qy | 2073 | CGGTGAAGCGGGAGCGCGCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTG | 2132 |
| Db | 1982 | CGGTGAAGCGGGAGCGCGCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTG | 2041 |
| Qy | 2133 | TGCCCTCATCCGAGCTGTCTTGCCACTGATGGAAGGACTCTCGACGGACCCAGACAGAAA | 2192 |
| Db | 2042 | TGCCCTCATCCGAGCTGTCTTGCCACTGATGGAAGGACTCTCGACGGACCCAGACAGAAA | 2101 |
| Qy | 2193 | CGTCTTCCCTGACGGAGAGCGTGTCTCTTTCAGGCTGGGTGAGGAGAACTCTCTG | 2252 |
| Db | 2102 | CGTCTTCCCTGACGGAGAGCGTGTCTCTTTCAGGCTGGGTGAGGAGAACTCTCTCTG | 2161 |
| Qy | 2253 | CCCTTCCCTTCAAGCTCCTCTTCTGGGTGATGCAAGCAGATCTTGGTTGCCGCGAGCT | 2312 |
| Db | 2162 | CCCTTCCCTTCAAGCTCCTCTTCTGGGTGATGCAAGCAGATCTTGGTTGCCGCGAGCT | 2221 |
| Qy | 2313 | ACACTGATGAACCTCCACGCGGTGCGCCCTTTGTAAACAAAACGAAAGAGTCTAAGCATTGC | 2372 |
| Db | 2222 | ACACTGATGAACCTCCACGCGGTGCGCCCTTTGTAAACAAAACGAAAGAGTCTAAGCATTGC | 2281 |
| Qy | 2373 | CACTTTA | 2379 |
| Db | 2282 | CACTTTA | 2288 |

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Job time : 1373.1 secs

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OM nucleic - nucleic search, using sw model

Run on: August 11, 2005, 00:22:23 ; Search time 420.208 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/ina/6B COMB.seq: *
5: /cgn2_6/prodata/1/ina/PTUS COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|----|----------------------|
| 1 | 2074.2 | 87.0 | 2319 | 4 | US-09-747-259-17 |
| 2 | 1873 | 78.6 | 3948 | 4 | US-09-799-451-125 |
| 3 | 71.4 | 3.0 | 3223 | 2 | US-08-620-694A-9 |
| 4 | 71.4 | 3.0 | 3223 | 3 | US-09-022-255-9 |
| 5 | 71.4 | 3.0 | 3223 | 3 | US-09-022-696-9 |
| 6 | 71.4 | 3.0 | 3223 | 3 | US-08-978-773-3 |
| 7 | 71.4 | 3.0 | 3223 | 3 | US-09-022-253-9 |
| 8 | 71.4 | 3.0 | 3223 | 3 | US-09-022-260-9 |
| 9 | 71.4 | 3.0 | 3223 | 3 | US-09-022-259-9 |
| 10 | 71.4 | 3.0 | 3223 | 3 | US-09-022-257-9 |
| 11 | 71.4 | 3.0 | 3223 | 4 | US-09-549-679-9 |
| 12 | 54.6 | 2.3 | 3288 | 2 | US-08-620-694A-1 |
| 13 | 54.6 | 2.3 | 3288 | 3 | US-09-022-255-1 |
| 14 | 54.6 | 2.3 | 3288 | 3 | US-09-022-696-1 |
| 15 | 54.6 | 2.3 | 3288 | 3 | US-08-978-773-1 |
| 16 | 54.6 | 2.3 | 3288 | 3 | US-09-022-253-1 |
| 17 | 54.6 | 2.3 | 3288 | 3 | US-09-022-260-1 |
| 18 | 54.6 | 2.3 | 3288 | 3 | US-09-022-259-1 |
| 19 | 54.6 | 2.3 | 3288 | 3 | US-09-022-257-1 |
| 20 | 54.6 | 2.3 | 3288 | 4 | US-09-549-679-1 |
| 21 | 45.2 | 1.9 | 72704 | 4 | US-09-902-540-1273 |
| 22 | 42.8 | 1.8 | 1263 | 4 | US-09-724-797-94 |
| 23 | 42.6 | 1.8 | 601 | 4 | US-09-949-016-200159 |
| 24 | 42.6 | 1.8 | 111509 | 4 | US-09-949-016-17379 |
| 25 | 42.4 | 1.8 | 1137 | 4 | US-09-902-540-8621 |
| 26 | 42.4 | 1.8 | 7982 | 4 | US-09-902-540-911 |
| 27 | 42.2 | 1.8 | 288 | 4 | US-09-489-039A-3694 |

| | | | | | | |
|------|------|-----|---------|---|----------------------|-------------------|
| 28 | 42.2 | 1.8 | 1749 | 4 | US-09-489-039A-3665 | Sequence 3665, Ap |
| c 29 | 42.2 | 1.8 | 3492 | 4 | US-09-489-039A-3882 | Sequence 3882, Ap |
| 30 | 41.4 | 1.7 | 1401 | 4 | US-09-489-039A-2359 | Sequence 2359, Ap |
| c 31 | 41.2 | 1.7 | 750 | 4 | US-09-902-540-1875 | Sequence 1875, Ap |
| 32 | 41.2 | 1.7 | 8030 | 4 | US-09-902-540-857 | Sequence 857, Ap |
| 33 | 41.2 | 1.7 | 10095 | 3 | US-08-822-586-45 | Sequence 45, Appl |
| c 34 | 41.2 | 1.7 | 20235 | 1 | US-07-642-734C-3 | Sequence 3, Appl |
| c 35 | 41.2 | 1.7 | 20235 | 3 | US-08-439-009A-3 | Sequence 3, Appl |
| 36 | 41.2 | 1.7 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appl |
| 37 | 41.2 | 1.7 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appl |
| c 38 | 41 | 1.7 | 357 | 4 | US-09-252-991A-10393 | Sequence 10393, A |
| c 39 | 41 | 1.7 | 1050 | 4 | US-09-252-991A-10765 | Sequence 10765, A |
| c 40 | 41 | 1.7 | 1437 | 4 | US-09-252-991A-10280 | Sequence 10280, A |
| 41 | 41 | 1.7 | 2448 | 4 | US-09-252-991A-10680 | Sequence 10680, A |
| 42 | 40.6 | 1.7 | 4041 | 3 | US-09-105-537-36 | Sequence 36, Appl |
| 43 | 40.6 | 1.7 | 36778 | 3 | US-09-105-537-5 | Sequence 5, Appl |
| 44 | 40.6 | 1.7 | 38506 | 3 | US-09-320-878-19 | Sequence 19, Appl |
| 45 | 40.6 | 1.7 | 38506 | 4 | US-09-141-908-1 | Sequence 1, Appl |

ALIGNMENTS

RESULT 1

US-09-747-259-17
; Sequence 17, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vanden, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1F1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/844,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24

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; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 17
; LENGTH: 2319
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-747-259-17

Query Match      87.0%; Score 2074.2; DB 4; Length 2319;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 3; Indels 39; Gaps 1;

QY 252 AGGGAGTGGGCCAGCCAGCAAGCAAGTGGGCTGTACAAATCACCTTCAAAATATGACA 311
DB 122 AGGGAGTGGGCCAGCCAGCAAGCAAGTGGGCTGTACAAATCACCTTCAAAATATGACA 181
QY 312 ATTGTACCACCTACTTTGAATCCAGTGGGCAAGCATGTATTGCTGACGCCCAGAAATATCA 371
DB 182 ATTGTACCACCTACTTTGAATCCAGTGGGCAAGCATGTATTGCTGACGCCCAGAAATATCA 241
QY 372 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCCACATTTCTTTGGTCCCGAGGG 431
DB 242 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCCACATTTCTTTGGTCCCGAGGG 301
QY 432 CCCTCGGCATCGAATTCCTGAAGGATTTCCGGTAATTAATCTCGAGGAGCTGAAGTCGGAGG 491
DB 302 CCCTCGGCATCGAATTCCTGAAGGATTTCCGGTAATTAATCTCGAGGAGCTGAAGTCGGAGG 361
QY 492 GAAGACAGTGCACCAATCTGATTCTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 551
DB 362 GAAGACAGTGCACCAATCTGATTCTTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAA 421
QY 552 GAATCGGAATGGAATCTCAACCTTTCTTGAATATGAAATTTGAAACGGATTTATTTCGTA 611
DB 422 GAATCGGAATGGAATCTCAACCTTTCTTGAATATGAAATTTGAAACGGATTTATTTCGTA 481
QY 612 AGTTTGCTCCCTTTCTTCCATTAATAAAGCAAGCAATTAACACCTTTCTTCTTTAGAA 671
DB 482 AGTTTGCTCCCTTTCTTCCATTAATAAAGCAAGCAATTAACACCTTTCTTCTTTAGAA 541
QY 672 CCCGAGCCTGTGACCTGTGTTTACAGCCGGACAAATCTAGCTTTGTAACCCCTTCTTGGAGC 731
DB 542 CCCGAGCCTGTGACCTGTGTTTACAGCCGGACAAATCTAGCTTTGTAACCCCTTCTTGGAGC 601
QY 732 CTCGGAACCTTGAACATCAGCCA-----753
DB 602 CTCGGAACCTTGAACATCAGCCAGCATGGCTCGGACATCGAGTGTCTTCGACCAAGCAC 661
QY 754 -GCATGGCTCGGACATGACGAGTGTCTTCGACCAATGCAACCGGACAACTTCGCGCTTCGTT 812
DB 662 CGCATGGCTCGGACATGACGAGTGTCTTCGACCAAGCAATTCGCGCTTCGCGTT 721
QY 813 TCTTCTATCTTCACTTACAGCTCAAGCAGCAAGGACCTTTCAAGCGAAGACCTGTGAAGC 872
DB 722 TCTTCTATCTTCACTTACAGCTCAAGCAGCAAGGACCTTTCAAGCGAAGACCTGTGAAGC 781
QY 873 AGGAGCAAACTACAGAGACGACCTGCTCTTCAAAAATGTTTCTCAGGGGATTTATA 932
DB 782 AGGAGCAAACTACAGAGATGACCTGCTCTTCAAAAATGTTTCTCAGGGGATTTATA 841
QY 933 TAAATTGAGCTGGTGAATGACATAACACAAAGAAAAGTGAATGATGATTCGCTTTAAGC 992
DB 842 TAAATTGAGCTGGTGAATGACATAACACAAAGAAAAGTGAATGATGATTCGCTTTAAGC 901
QY 993 CAGTGCACTCCCGTGGGCCGGCCCATCAGAGCGCTGGCCATCACAGTGCACCTGGTAG 1052
DB 1052 CAGTGCACTCCCGTGGGCCGGCCCATCAGAGCGCTGGCCATCACAGTGCACCTGGTAG 2041

902 CAGTGCACTCCCGTGGGCCGGCCCATCAGAGCGCTGGCCATCACAGTGCACCTGGTAG 961
1053 TCATATCGGCATTTCCGACGCTCTTCACTGTGATGTGCGCAAGCAACAAAGAAATA 1112
962 TCATATCGGCATTTCCGACGCTCTTCACTGTGATGTGCGCAAGCAACAAAGAAATA 1021
1113 TATATTACACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA 1172
1022 TATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAA 1081
1173 GAGAGAGCTCCGCGCCGCGCGCGAAGGTCTTCTGCTATTTCCAGTAAAGATGGCCAGA 1232
1082 GAGAGAGCTCCGCGCCGCGCGCGAAGGTCTTCTGCTATTTCCAGTAAAGATGGCCAGA 1141
1233 ATCATATGAATGTGCTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1292
1142 ATCATATGAATGTGCTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGG 1201
1293 TGGCTCTGGACCTCTGTGGAAAGACTTTCAGCCCTCTGTAGAGAGGCGCAGAGAAATGGGTCA 1352
1202 TGGCTCTGGACCTCTGTGGAAAGACTTTCAGCCCTCTGTAGAGAGGCGCAGAGAAATGGGTCA 1261
1353 TCCAGAGAGATCCAGAGTCCCGAGTTCATCATTTGTGTTTGTTCAAAAGGTATGAAGTACT 1412
1262 TCCAGAGAGATCCAGAGTCCCGAGTTCATCATTTGTGTTTGTTCAAAAGGTATGAAGTACT 1321
1413 TTGTGGAACAAGAAACTACAAACAACAAGAGAGTGGCGGAGGCTCGGGGAAAGAGAGAC 1472
1322 TTGTGGAACAAGAAACTACAAACAACAAGAGAGTGGCGGAGGCTCGGGGAAAGAGAGAC 1381
1473 TCTTCTGTGTGGGCTGTGAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGCAGAGTTCGT 1532
1382 TCTTCTGTGTGGGCTGTGAGCCATTCGCGAAAGCTCCGCGAGGCGCAAGCAGAGTTCGT 1441
1533 CCGCGGCGCTCAGCAAGTTCATTCGCGCTCTACTTTGATTTATTCCTGCGAGGAGACGTC 1592
1442 CCGCGGCGCTCAGCAAGTTCATTCGCGCTCTACTTTGATTTATTCCTGCGAGGAGACGTC 1501
1593 CCGGTATCTTAGACTGAGTACCAAGTACAGATCATGAGCAATCTTCTCAGCTCTGTT 1652
1502 CCGGTATCTTAGACTGAGTACCAAGTACAGATCATGAGCAATCTTCTCAGCTCTGTT 1561
1653 CCACATTCGACTCTCCGAGACCAAGGCTCCAGGAGCGGGGAGCAGACACGCGACAGAGCA 1712
1562 CCCACTCTGACTCTCCGAGACCAAGGCTCCAGGAGCGGGGAGCAGACACGCGACAGAGCA 1621
1713 GCAGAGAGAACTACTTCCGAGAGCAAGTCCAGGCTCCCTATACGTCGCCATTTGCAACA 1772
1622 GCAGAGAGAACTACTTCCGAGAGCAAGTCCAGGCTCCCTATACGTCGCCATTTGCAACA 1681
1773 TGCAACAGTTCATTTGACAGAGGCGCGACTGGTTGGAAGAGCAGTTCGTTCCCTTCATC 1832
1682 TGCAACAGTTCATTTGACAGAGGCGCGACTGGTTGGAAGAGCAGTTCGTTCCCTTCATC 1741
1833 CTCTCTCAGCTGCGCTACCGGAGCGCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1892
1742 CTCTCTCAGCTGCGCTACCGGAGCGCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAA 1801
1893 ATGATGTTCATGTGCAAAACACAGGCGCTGAGAGTGAATTCCTGCTAAAGGTAGAGCGGCTG 1952
1802 ATGATGTTCATGTGCAAAACACAGGCGCTGAGAGTGAATTCCTGCTAAAGGTAGAGCGGCTG 1861
1953 TTTTGGGGCAACCGGACCAAGCGCACTCCAGCAAGCAAGAGTCAAGTGGGGGCTTGAGCC 2012
1862 TTTTGGGGCAACCGGACCAAGCGCACTCCAGCAAGCAAGAGTCAAGTGGGGGCTTGAGCC 1921
2013 AAGACGGGGAGCGCGGCTGCGCTTCAAGTACGCGCGCTCCAGCCCTGCTGCAACA 2072
1922 AAGACGGGGAGCGCGGCTGCGCTTCAAGTACGCGCGCTCCAGCCCTGCTGCAACA 1981
2073 CGGTGAAAGCGCGGAGCGGCTTCCGACATGCGCGGGGAGCTCAGGCACTCTATGACTCGTCTG 2132
1982 CGGTGAAAGCGCGGAGCGGCTTCCGACATGCGCGGGAGCTCAGGCACTCTATGACTCGTCTG 2041
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| | | | |
|----|------|---|------|
| QY | 2133 | TGCCCCATCCGAGCTGTCTCTGCACTGATGGAAGGACTCTCGACGACGACAGAGAA | 2192 |
| Db | 2042 | TGCCCCATCCGAGCTGTCTCTGCACTGATGGAAGGACTCTCGACGACGACAGAGAA | 2101 |
| QY | 2193 | CCTCTTCCCTGACGAGAGCGTGTCTCTCTTTCAGGCGCTGGGTGAGAGAACTCTCTG | 2252 |
| Db | 2102 | CCTCTTCCCTGACGAGAGCGTGTCTCTCTTTCAGGCGCTGGGTGAGAGAACTCTCTG | 2161 |
| QY | 2253 | CCCTTCCCTTCCAAAGCTCTCTCTCTGCGTCAATGCAAAAGCAGATCTTGGTTCGCGCAGT | 2312 |
| Db | 2162 | CCCTTCCCTTCCAAAGCTCTCTCTCTGCGTCAATGCAAAAGCAGATCTTGGTTCGCGCAGT | 2221 |
| QY | 2313 | ACACTGATGAATCCACGCGGTGCGCCCTTTTGTAAACAAAGAGCTTAAGCAATTGC | 2372 |
| Db | 2222 | ACACTGATGAATCCACGCGGTGCGCCCTTTTGTAAACAAAGAGCTTAAGCAATTGC | 2281 |
| QY | 2373 | CACCTTTA 2379 | |
| Db | 2282 | CACCTTTA 2288 | |

RESULT 2

US-09-799-451-125

; Sequence 125, Application US/09799451

; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhang, Jie

; APPLICANT: Xue, Aidong J.

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Ma, Yunging

; APPLICANT: Yamazaki, Victoria

; APPLICANT: Chen, Rui-hong

; APPLICANT: Wang, Zhiwei

; APPLICANT: Wang, Dunrui

; APPLICANT: Yang, Yonghong

; APPLICANT: Wehrman, Tom

; APPLICANT: Ghosh, Reena

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6783969el Nucleic Acids and

; FILE REFERENCE: Polypeptides

; CURRENT APPLICATION NUMBER: US/09/799,451

; CURRENT FILING DATE: 2001-03-05

; NUMBER OF SEQ ID NOS: 948

; SOFTWARE: pt_FL_genes Version 2.0

; SEQ ID NO 125

; LENGTH: 3948

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (60)..(1844)

US-09-799-451-125

| | | | | |
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| Query Match | 78.6%; | Score 1873; | DB 4; | Length 3948; |
| Best Local Similarity | 99.7%; | Pred. No. 0; | | |
| Matches 1876; | Conservative | 0; | Mismatches | 5; |
| | | | Indels | 0; |
| | | | Gaps | 0; |
| QY | 503 | CAACAACTGATTTCTAAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATG | 562 | |
| Db | 3 | CCAAACTGATTTCTAAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATG | 62 | |
| QY | 563 | GAATCTCAACCTTCTGTAATATGAAATTTGAAACCGGATTTATTCGTAAGGTTGTCCCT | 622 | |
| Db | 63 | GAATCTCAACCTTCTGTAATATGAAATTTGAAACCGGATTTATTCGTAAGGTTGTCCCT | 122 | |


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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/410,535
;; FILING DATE: 23 MARCH 1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,695
;; REFERENCE/DOCKET NUMBER: 2617-B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3223 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; STRAIN: IL-17 R (hCTLA8 receptor)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 93..2693
;;
;; US-09-022-696-9
Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCGTCAGTGTTTCGCTACTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295
DB 1264 ACGTGGACGTGCTCGCAATTCGCCACATGTTCTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1323
QY 1296 CTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAAATGGGTCTATCC 1355
DB 1324 CCCTGGACCTGTGGAAGAGCAGGCCATCTCGGAGGCGAGGAGTCTATGACCTGGGTGGGCC 1383
QY 1356 AGAAGATCCAGGATCCAGTTC-----ATCATTGTGTTTGTTCCTCCAAAGTA 1403
DB 1384 GTCAGAACGAGAGATGTTGGAGAGCAACTCTAAGATCATGCTCTGTGCTCCCGCGCA 1443
QY 1404 TGAAGTACTTTGTGGAAGAAGAACTACAACACAAAGAGGTGGCGAGGCTCGGGGA 1463
DB 1444 CGCGCGCAAGTGGCAGCGCTCTCTGGCGCGGGGGCGCTGTGCGGCTGCGCTCGCACC 1503
QY 1464 AAGGAGAGCTCTCTCTGTGGCGGTGTGAGCAATTCGCCAAAGCTCGCCAGGCGCAAGC 1523
DB 1504 ACGGAAAGCCGTGGGGAGCTGTTCACTGAGCGCATGAATGATCTCTCCGAGCTTCA 1563
QY 1524 AGAGTTCCTCGCGCGCTCAGCAAGTTTATCGCGCTCTACTTTGATTATTCCTCGCAGG 1583
DB 1564 AGAGCGACCTGCTCTCGGACCTACGTAGTCTGTACTTTCAGCGAGTCTGAGTGTGAGC 1623
QY 1584 GAGAGTCTCCCGGTATCTCTAGACCTGAGTACCAAGTACAGACTCATGAGCAATCTTCCTC 1643
DB 1624 GCGACGTCTCCGACCTGTTTCGCGCGCGCGCGGTACCGCTCATGACAGGTTTCGAGG 1683
QY 1644 AGCTCTGTTCCCACTTGCACCTCCGAGACACCGGCTCCAGGAGCGCGGGCAGACACGC 1703
DB 1684 AGGTGACTTCCGATTCAGGACCTGGAGATGTTCCAGCCGGCGCGCATGACCCCGGTAG 1743
QY 1704 GACAGGGCAGCAGAGGAAGTAATCTTCGAGCAAGTTCAGCGCGGTTCCTATACGTTCGCCA 1763
DB 1744 GGGAGCTGTGCGGGGACAACTACCTGCGAGCGCGCGGCGGAGCAGCTCCGCGCGCGCC 1803
QY 1764 TTGCAACATGACCAAGTTTATGACAGGAGCGCCGACTGGTTTGAAAGCAGTTTCGTTTC 1823
DB 1804 TGGACAGGTTCCGGGACTGGCAGGTCCGCTGTCCGAGTGTTCGAATGTGAGAACTCT 1863
QY 1824 CCT 1826

;; RESULT 6
;; US-08-978-773-3
;; Sequence 3, Application US/08978773
;; Patent No. 6083906
;; GENERAL INFORMATION:
;; APPLICANT: Troutt, Anthony
;; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple PowerMacintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/978,773
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/052,525
;; FILING DATE: 27 NOVEMBER 1996
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2623-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3223 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Human
;; IMMEDIATE SOURCE:
;; CLONE: IL-17R
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 93..2690
;;
;; US-08-978-773-3
Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCGTCAGTGTTTCGCTACTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295
DB 1264 ACGTGGACGTGCTCGCAATTCGCCACATGTTCTCTCCAGGACTTCTGTGGCTGTGAGGTGG 1323
QY 1296 CTCTGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAGGGCAGAGAAATGGGTCTATCC 1355
DB 1324 CCCTGGACCTGTGGAAGAGCAGGCCATCTCGGAGGCGAGGAGTCTATGACCTGGGTGGGCC 1383
QY 1356 AGAAGATCCAGGATCCAGTTC-----ATCATTGTGTTTGTTCCTCCAAAGTA 1403
DB 1384 GTCAGAACGAGGAGATGTTGGAGAGCAACTCTAAGATCATGCTCTGTGCTCCCGCGCA 1443
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QY 1404 TGAAGTACTTTGTGCAAGAGAACTACAAACAAAGAGAGTGGCGAGGCTCGGGA 1463
Db 1444 CGCGCGCAAGTGGCAGCGCTCTGGGCGGGGGCGCTGTGGCTGCGGACC 1503
QY 1464 AAGGAGAGCTTTCTGTGGGGTGTGAGCCATTGCCGAAAGCTCCGAGGCGCAAGC 1523
Db 1504 ACGGAAAGCCGTGGGGACCTGTTCACTGCAGCCATGAACATGATCTCCGGAATTCA 1563
QY 1524 AGAGTTCTGTCGGCGGCTCAGCAAGTTTATGCGCGTCTACTTTGATTATTCCTGCGAGG 1583
Db 1564 AGAGCCAGCTGTCTCGGCACTTCTGCGCACTACGAGTCTGTACTTACGCGAGTGTGAGC 1623
QY 1584 GAGAGTCCCGGATCTTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTC 1643
Db 1624 GCGAGTCCCGACCTGTTGCGCGCGCGCGGTACCGCTCATGACAGGTTGAGG 1683
QY 1644 AGCTGTGTTCCACTTGTGACTCCGAGACCGGCTCAGAGCGGGGCGAGCACGCG 1703
Db 1684 AGGTGTACTTCCGCATCCAGGACCTGGAGATGTTCCAGCGCGGCGCATGCAACGCGTAG 1743
QY 1704 GACAGGCGAGCAGAGGAACTACTTCCGAGCAAGTCAAGCGGTCCTATACGTCGCA 1763
Db 1744 GCGAGCTGTGCGGGGAGAACTACTTCCGAGCGCGGCGGCGAGGCTCCGCGCGGCC 1803
QY 1764 TTTGCAACATGACACAGTGTATTTAGAGAGGAGCCGACTGTTGAAAGAGCAGTTCTGTT 1823
Db 1804 TGGACAGTTCCGGAGTGGCAGGTCGCTGTCCGACTGTTGGAATGTGAGAACCTCT 1863
QY 1824 CCT 1826
Db 1864 ACT 1866

RESULT 7

US-09-022-253-9
; Sequence 9, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human
; STRAIN: IL-17 R (hCTLA8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93...2693
; US-09-022-253-9

Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;
QY 1236 ACATGAATGTGTCAGTGTTCGCTACTTCTCCAGGACTTCTGTGCTGTGAGGTGG 1295
Db 1264 ACGTGGAGCTGCTCGAAATTCGCCAGTTCCTGCTCACCGCTGCGGACGGAAGTGG 1323
QY 1296 CTCTGGACCTGTGGAGAGACTTTCAGCCCTCTGTAGAGAGGCGAGAGAAATGGGTATCC 1355
Db 1324 CCTGGACCTCTGGAAGAGCAGGCAATCTCGAGGCGAGGAGTCAATGACCTGGGTGGGCC 1383
QY 1356 AGAAGATCCAGAGTCCAGTTC-----ATCATTGTGTTTGTTCCTCAAGGTA 1403
Db 1384 GTGAGAGCAGAGATGTGTGAGAGCAACTCTAAGATCATGCTCTGTGCTCCCGCGCA 1443
QY 1404 TGAAGTACTTTGTGACAAAGAACTAACAACAAGAGAGTGGCGAGGCTCGGGA 1463
Db 1444 CGCGCGCAAGTGGCAGCGCTCTCGGCGCGGGGCGCTGTGCGGCTGCGCTCGGACC 1503
QY 1464 AAGGAGAGCTTCTCTGTGGGGTGTGAGCAATTCGCAAGCTCCGCAAGCTCCGAGGCGCAAGC 1523
Db 1504 ACGGAAAGCCGTGGGGGACCTGTTCACTGAGGCAATGAACATGATCTCTCCGGAATTCA 1563
QY 1524 AGAGTTGTCGCGCGGCTCAGCAAGTTTATCGCGTCTACTTTGATTATTCCTCGGAGG 1583
Db 1564 AGAGCCAGCTGTCTCGGCACTACGAGTCTGTACTTTAGCGAGGTCAGCTGTGAGC 1623
QY 1584 GAGAGTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCCTC 1643
Db 1624 GCGAGTCCCGACCTGTTGCGCGCGCGCGGTACCGCTCATGAGCAGGTTGAGG 1683
QY 1644 AGCTGTGTTCCACTTGTGACTCCCGAGACCGGCTCAGGAGCGGGGCGAGCACAGC 1703
Db 1684 AGGTGTACTTCCGATCCAGGACCTGGAGATGTTCCAGCGGGGCGCATGACCCCGTAG 1743
QY 1704 GACAGGCGAGCAGAGGAACTACTTCCGAGCAAGTCAAGCGGTCCTTATACGTCGCA 1763
Db 1744 GCGAGCTGTGCGGGGAGCACTACCTGCGAGCGCGGGGCGGAGGAGCTCCGCGCGGCC 1803
QY 1764 TTTGCAACATGACCAAGTTTATTTAGAGAGGCGGAGTGTTCGAAAGAGCAGTTCGTT 1823
Db 1804 TGGACAGTTCCGGGACTGGCAGGTCGCTGTCCGAGTGGTTCGAAATGTGAGAACCTCT 1863
QY 1824 CCT 1826
Db 1864 ACT 1866

RESULT 8

US-09-022-260-9
; Sequence 9, Application US/09022260
; Patent No. 6100235

LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93...2693
US-09-022-259-9

Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCCTCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGTGG 1295
DB 1264 AGTGGACGTGTCTGAAATTCGCCAGTCTCTGTCTACCCCTGCGGCACGGAAGTGG 1323

QY 1296 CTCCTGACCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGGCAGAGAAATGGGTATCC 1355
DB 1324 CCTGGACCTGTGGAAGAGCAGGCCATCTCGGAGCGAGGAGTCATGACCTGGTGGGCC 1383

QY 1356 AGAAGATCACAGATCCCGCTTC-----ATCATTTGTTGTTTCCAAAGGTA 1403
DB 1384 GTCAAGCAGGAGGATGTTGGAGAGCACTCTAAGATCATCTGTCTCTCCCGCGCA 1443

QY 1404 TGAAGTACTTGTGGACAGAAAGACTACAAACAAAGAGGCTGGCGAGCTCGGGGA 1463
DB 1444 CGCGGCCAAGTGGCAGCGCTCTTGGGCGGGGGGGCGCTGTGGCTGCGCTCGGACC 1503

QY 1464 AAGGAGAGCTCTTCTGTGGCGGTGTACGCCATTTGCGAAAGCTCCGCCAGGCCAAGC 1523
DB 1504 ACGGAAGCCCGTGGGGACCTGTTCACTGACGCCATGAATGATCTCTCCCGACTTCA 1563

QY 1524 AGAGTTGTCGCGGGGCTCAGCAGATTTATCGCGTCTACTTTGATTTATCTCTGGAGG 1583
DB 1564 AGAGGCCAGCTGCTTCGGCACCTAGTAGTCTGTCTACTTTCAGCGAGGTTCAGCTGTGAG 1623

QY 1584 GAGAGCTCCCGGTATCTTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTC 1643
DB 1624 GCGAGCTCCCGACCTGTTTCGGCGCGCGCGCGGTACCCGCTCATGACAGGTTGAGG 1683

QY 1644 AGCTCTGTTCCCACTTGCACTCCGAGACACGGCCCTCCAGGAGCGCGGCGAGCACGCG 1703
DB 1684 AGGTGACTTCCGCATCCAGGACCTGGAGATGTTCCAGCGCGCGCATGCACCGGTAG 1743

QY 1704 GACAGGCGACGAGAAAGAACTACTTCCGAGCAAGTTCAGGCGGCTCCCTATAGTCGCCA 1763
DB 1744 GGGAGCTGTGGGGGACAACTACTTCCGAGGCGCGGGCGGAGGAGCTCCGCGCGCGCC 1803

QY 1764 TTTGCAATGACCACTTTATGACGAGGCGCGGAGCTGTTGCAAGAGTTCGTTTC 1823
DB 1804 TGGACAGGTTCGGGAGCTGGCAGGTCCTGTGTCCCGACTGGTTCGAATGTGAACTCT 1863

QY 1824 CCT 1826
DB 1864 ACT 1866

RESULT 10
US-09-022-257-9
Sequence 9, Application US/09022257
Patent No. 6197525
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93...2693
US-09-022-257-9

Query Match 3.0%; Score 71.4; DB 3; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCCTCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGTGG 1295
DB 1264 AGTGGACGTGTCTGAAATTCGCCAGTCTCTGTCTACCCCTGCGGCACGGAAGTGG 1323

QY 1296 CTCCTGACCTGTGGGAAGACTTTCAGCTCTGTAGAGAGGGCAGAGAAATGGGTATCC 1355
DB 1324 CCTGGACCTGTGGAAGAGCAGGCCATCTCGGAGCGAGGAGTCATGACCTGGTGGGCC 1383

QY 1356 AGAAGATCCAGGTCCTCAGTTC-----ATCATTTGTTGTTTCCAAAGGTA 1403
DB 1384 GTCAAGCAGGAGGATGTTGGAGAGCACTCTAAGATCATCTGTCTCTCCCGCGCA 1443

QY 1404 TGAAGTACTTGTGGACAGAAAGAACTACAAACAAAGAGGTTGGCCAGGCTCGGGGA 1463
DB 1444 CGCGGCCAAGTGGCAGCGCTCTCTGGGCGCGGGCGCGCTGTGGCTGCGCTCGGACC 1503

QY 1464 AAGGAGAGCTCTTCTGTGGCGGTGTGAGCCATTTGCCGAAAGCTCCGCCAGGCCAAGC 1523
DB 1504 ACGGAAGCCCGTGGGGACCTGTTCACTGACGCCATGAATGATCTCTCCCGACTTCA 1563

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QY 1524 AGAGTTCTGTCGCGCGCTCAGCAAGTTTATCGCGTCTACTTTGATTATTTCCTGCGAGG 1583
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Db 1564 AGAGCCAGCTGTTCGGCACCTACGAGTCTGCTACTTACGAGAGTCACTGTGACG 1623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1584 GAGAGTCCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCCTC 1643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1624 GCGAGTCCCCGACCTGTTCGGCGCGCGCGCGGTACCCGCTCATGACAGGTTTCGAGG 1683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1644 AGCTCTGTTCCTACCTGCACTCCGAGACACAGGCTCCAGAGCGCGGGGAGACACGC 1703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1684 AGGTGTACTCCGATCCAGGACCTGAGATGTTCCAGCCGCGCGCATGACACCGCGTAG 1743
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1704 GACAGGGCAGCAGAGGAACTTCCGAGCAAGTCAAGCGCGTCCCTATACGTCGCA 1763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1744 GGGAGCTGTGGGGGACAACTACCTGCGGAGCCCGGGCGGAGGAGCTCCGCGCGCGCC 1803
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QY 1764 TTTGCAACATGACACAGTTTATTGACGAGGAGCCCGACTGGTTTGAAAGCAGTTTCGTT 1823
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Db 1804 TGGACAGTTCCGGGACTGGCAGTCCGCTGTCCGACTGGTTGCAATGTGAGAACCTCT 1863
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1824 CCT 1826
    |||||
Db 1864 ACT 1866
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RESULT 11
US-09-549-679-9
; Sequence 9, Application US/09549679
; Patent No. 6680057
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; Spriggs, Melanie
; Fanslow, William
; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,679
; FILING DATE: 14-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
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; ORGANISM: Human
; STRAIN: IL-17 R (hCTLA8 receptor)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 93..2693
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-549-679-9

Query Match      3.0%; Score 71.4; DB 4; Length 3223;
Best Local Similarity 46.4%; Pred. No. 1.7e-09;
Matches 280; Conservative 0; Mismatches 311; Indels 12; Gaps 1;

QY 1236 ACATGAATGTCGTTCAGTGTTCGCTTACTTCCTCCAGGACTTCTGTGGCTGTGAGGTGG 1295
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Db 1264 ACGTGGACGTGCTCTGAATTCGCCAGTTCCTGTCTCA CGCCTGCGGCACGGAAGTGG 1323
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QY 1296 CTCTGGACCTGTGTGGGAAGACTTTCAGCTCTGTGTAGAGAGGCGACAGAGAAATGGGTATCC 1355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1324 CCCTGGACCTGTCTGAAGAGCAGGCCCATCTCGAGGCGAGGAGTCATGACCTGGGTGGGCC 1383
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QY 1356 AGAAGATCCAGAGTCCAGTTC-----ATCATTTGTGTTTGTTCGAAGGTA 1403
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Db 1384 GTCAGAAGCAGGAGATGTTGGAGAGCAACTCTAAGATCATGCTCTGTGCTCCCGCGCA 1443
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QY 1404 TGAAGTACTTTGTGCAACAAGAAACTACAACACAAAGGAGGTGGCGAGGCTCGGGGA 1463
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Db 1444 CGCGCGCAAGTGCAGGCGCTCCTGGGCGGGGGGCGCTGTGCGGCTGCGCTCGGACC 1503
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QY 1464 AAGGAGAGCTCTTCTCTGTGGCGGTGTGAGCAATTTGCCGAAAAGTCTCGGCAGGCGCAAGC 1523
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Db 1504 ACGGAAAGCCGCTGGGGGACCTGTTCACTGCGAGCCATGAACATGATCTCTCCCGACTTCA 1563
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QY 1524 AGAGTTGTCGCGCGGCTCAGCAAGTTTATCGCGCTACTTTGATTATTTCCTGCGAGG 1583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1564 AGAGCCAGCCTGCTTCGGCACCTACGTAAGTCTGCTACTTTCAGGAGGTCAAGTGTGACG 1623
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QY 1584 GAGAGCTCCCGGTATCTAGACCTGAGTACCAAGTACAGACTCATGGACAATTTCTCTC 1643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1624 GCGAGTCCCCGACCTGTTGCGCGCGCGCGCGGTACCCGCTCATGACAGGTTTCGAGG 1683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1644 AGCTCTGTTCCTACTTCCGAGACCAACGCGCTTCAGAGCGCGGGGAGCACACGC 1703
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Db 1684 AGGTGTACTTCGCGCATCCAGGACCTGGAGATGTTCCAGCGCGGCGCATGACCGCGTAG 1743
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QY 1704 GACAGGCGAGCAGAGGAACTACTTCCGAGCAAGTCAAGCGCGTCCCTATACGTCGCA 1763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1744 GGGAGCTGTTCGGGGGACAACTACTTCCGAGGAGCCCGGGCGGAGGAGCTCCGCGCGCGCC 1803
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QY 1764 TTTGCAACATGCACCAAGTTTATTGACGAGGAGCCCGACTGGTTTGAAAGCAGTTCGTT 1823
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Db 1804 TGGACAGTTCCGGGACTGGCAGTCCGCTGTCCGACTGGTTGCAATGTGAGAACCTCT 1863
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QY 1824 CCT 1826
    |||||
Db 1864 ACT 1866

RESULT 12
US-08-620-694A-1
; Sequence 1, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
```

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; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-08-620-694A-1

Query Match 2.3%; Score 54.6; DB 2; Length 3288;
Best Local Similarity 48.0%; Pred. No. 0.00011;
Matches 156; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 1503 AAAAGCTCGCGCAGCCAGCAGAGTTGCTCCGCGCGCTCAGCAAGTTTATCGCGTCT 1562
DB 1580 ACATGATCTGCCAGACTTCAAGAGCCAGCTGCTTCGGCACCTACGTTGTTGCTACT 1639
QY 1563 ACTTTGATTATTCCTCGCGAGGAGACGTCCTCCGATTCCTAGACCTGAGTACCAAGTACA 1622
DB 1640 TCAGTGGCATCTGTAGTGAGAGGGATGTCCTTCAACATCACCTCCAGGTACC 1699
QY 1623 GACTCATGGACAATCTTCTCAGCTCTGTTCCACTTCCGAGACCCAGGCTCC 1682
DB 1700 CACTCATGGACAATCTTCCGAGGTTTACTTCCGATCCAGACCTGGAGATGTTTGAAC 1759
QY 1683 AGGAGCCGGGCGAGCAGCAGCGAGGAGGAGGAACTACTTCCGAGCAAGTACAG 1742
DB 1760 CCGGCGGATGACCATGTGACAGAGCTCAGAGGAGCAATTAACCTGCAGAGCCCTAGTG 1819
QY 1743 GCGCGTCCCTATACGTGCGCAATTTGCAATGCACGAGTTTATGACGAGGAGCCGACT 1802
DB 1820 GCGGCGAGCTCAAGGAGGCTGTGTTAGGTTCCAGGAGTGCGCAAAACCCAGTCCCGGACT 1879
QY 1803 GGTTCGAAAAGCAGTTCTGTTCCCTT 1827
DB 1880 GGTTCGAGCGTGAGAACCTCTGCTT 1904

RESULT 13
US-09-022-255-1

; Sequence 1, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715
; US-09-022-255-1

Query Match 2.3%; Score 54.6; DB 3; Length 3288;
Best Local Similarity 48.0%; Pred. No. 0.00011;
Matches 156; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 1503 AAAAGCTCGCGCAGCCAGCAGAGTTGCTCCGCGCGCTCAGCAAGTTTATCGCGTCT 1562
DB 1580 ACATGATCTGCCAGACTTCAAGAGCCAGCTGCTTCGGCACCTACGTTGTTGCTACT 1639
QY 1563 ACTTTGATTATTCCTCGCGAGGAGACGTCCTCCGATTCCTAGACCTGAGTACCAAGTACA 1622
DB 1640 TCAGTGGCATCTGTAGTGAGAGGGATGTCCTTCAACATCACCTCCAGGTACC 1699
QY 1623 GACTCATGGACAATCTTCTCAGCTCTGTTCCACTTCCGAGACCCAGGCTCC 1682
DB 1700 CACTCATGGACAATCTTCCGAGGTTTACTTCCGATCCAGACCTGGAGATGTTTGAAC 1759
QY 1683 AGGAGCCGGGCGAGCAGCAGCGAGGAGGAGGAACTACTTCCGAGCAAGTACAG 1742
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Db 1760 CCGCGCGATGACCATGTCAGAGAGCTCACAGGGGCAATACCTGCGAGAGCCCTAGTG 1819
Qy 1743 GCCGGTCCCTATACGTCCGCCATTTGCAACATGACACAGTATTATTGACAGAGAGCCCGACT 1802
Db 1820 GCCGCGACTCAAGGAGGCTGTGCTTAGGTTCCAGGAGTGGCAAAACCCAGTGGCCCGACT 1879
Qy 1803 GGTTCGAAAGCAGTTCGTTCCTT 1827
Db 1880 GGTTCGAGCGTGAGAACCTCTGCTT 1904

RESULT 14

US-09-022-696-1
; Sequence 1, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995

CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; STRAIN: HVS13 receptor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 121..2715

US-09-022-696-1
Query Match 2.3%; Score 54.6; DB 3; Length 3288;
Best Local Similarity 48.0%; Pred. No. 0.00011;
Matches 156; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 1503 AAAAGCTCCGCGAGGCAAGCAGAGATTGTCGCGCGCGCTCAGCAAGTTTATCGCCGTCT 1562
Db 1580 ACATGATCTCGCCAGACTTCAAGAGGGCCAGCGCTGCTCGGCACTTACGTTGTTGCTACT 1639
Qy 1563 ACTTTGATTATTCCTCGAGGGAGACGTCCCGGTATCTTAGACTGAGTACCAAGTACA 1622
Db 1640 TCAGTGGCATCTGTAGTGAGAGGGATGTCGCCGACCTCTTCAACATCACTCCAGGTACC 1699
Qy 1623 GACTCATGGACAATCTTCTCAGCTCTGTTCCCACTTGCACCTCCGGAGACCACGGCCTCC 1682
Db 1700 CACTCATGGACAGATTTGAGAGGTTTACTTCCGGATCCAGGACCTGGAGATGTTGAAC 1759
Qy 1683 AGGAGCCGGGCGAGCACACGCGACAGGGCGAGCAGAAGAACTACTTCCGGAGCAAGTCAG 1742
Db 1760 CCGCCCGATGCACCATGTGAGAGGCTCAGAGGACATTACTGAGAGCCCTAGTG 1819
Qy 1743 GCGGTCCCTATACGTCCGCCATTTGCAACATGACACAGTATTATTGACAGAGAGCCCGACT 1802
Db 1820 GCCGCGACTCAAGGAGGCTGTGCTTAGGTTCCAGGAGTGGCAAAACCCAGTGGCCCGACT 1879
Qy 1803 GGTTCGAAAGCAGTTCGTTCCTT 1827
Db 1880 GGTTCGAGCGTGAGAACCTCTGCTT 1904

RESULT 15

US-08-978-773-1
; Sequence 1, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Trout, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2623-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mouse
; IMMEDIATE SOURCE:

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OM nucleic - nucleic search, using sw model

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(without alignments)
10857.712 Million cell updates/sec

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Perfect score: 2383
Sequence: 1 ccgcgcggccaccgccac.....aagcattgccacttagctg 2383

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_hic:*
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8: gb_gsal:*
9: gb_gsal2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 18 | 384.6 | 16.1 | 680 | 5 | BU267653 BU267653 |
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ALIGNMENTS

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AY408489
VERSION
AY408489.1 GI:39764460
KEYWORDS
GSS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1677)
AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
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VERSION AY408490.1 GI:39764461
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1677)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1677)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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genomic survey sequence.
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VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE

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| source | | | |


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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Laver and broiler"
/db_xref="taxon:9031"
/clone="CHST828k13"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRN22"
/Note="Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN
Query Match 17.6%; Score 420.2; DB 5; Length 717;
Best Local Similarity 76.3%; Pred. No. 8.6e-106;
Matches 530; Conservative 0; Mismatches 163; Indels 2; Gaps 1;

QY 923 GGGGATTATATTAATGAGCTGTGATGACACTAACAACAAGAAAAGTGATGATAT 982
DB 3 GGGGATTATATCATCGAGCTGTGATGACACTATATACACAAGAAAACATGCACTAT 62

QY 983 GCCTTAAAGCCAGTCACTCCCGTGGCGCGGCCCATCAGAGCCGTGGCCATCAAGTG 1042
DB 63 GCCTTAAAGCCAGTCACTCCCGTGGCGCGGCCCATCAGAGCTATTTGCCATTAAGTGC 122

QY 1043 CCATCGGTAGTATATCGGCATTCGGAGCTTCCTGATGATGATGCGGCAAGAGCA 1102
DB 123 CTTTATGTTGTCTATTCGGCATTTTCAACACTTTTTCACAGTGTATGCGGCAAAAGCAG 182

QY 1103 CAAGAAAATATATTTTCACTTTAGATGAAGAGAGCTCTGAGTCTTCCACATACACTGCA 1162
DB 183 CAAGAAAATATATTTTCCATCTAGACGAGAGAGCTCAGATCTTCAGCTTATGGTGA 242

QY 1163 GCACATCCCAAGAGAGAGGCTCCGGCGCGCGCGCGAAGGTTCTTCTGCTATTTCCAGTAA 1222
DB 243 GGTCTCCCTGTGAAAGACTTCGCCCGCGCGCGCAAAAGTATTCATCTGCTATTTCCAGTAA 302

QY 1223 GATGCGCAGAAATCAATGAATGTGTCAGTGTTTGGCTTCTGCTATTCATCTGCTCAGGACTTCTGT 1282
DB 303 GATGCGCAGAAACATTAATGTATTCAGTGTCTTATTTCTTATTTCTCCAGGACTTCTGT 362

QY 1283 GCCTGTGAGTGGCTCTGACCTGTGGAGAGACTTCAGCTCTGTAGAGAGCGGAGAGA 1342
DB 363 GCCTGTGAGTGGCTCTGAGTTGTGGGAAGATCTGAAATTTGTAAAGAAAGTCAGAAA 422

QY 1343 GAATGGGTCTATCCAGAAAGATCCACGAGTCCCGAGTTCATCATTTGTGGTTTGTTCCTCAAGGT 1402
DB 423 GAATGGGTCTATTAAGAAATTAATGAGTCTCAGTTTATCATCATTTGTGTGCTCCAAGGA 482

QY 1403 ATGAAGTACTTTGTGGAAGAAGAACTACAACAAGAGAGTGGCGGAGCTCGGG 1462
DB 483 ATGAAGTACTTTGTGGAAGAAAGAAATTTGAAACACAGAGGAGTAAACAAAGACACAGGG 542

QY 1463 AAAGAGAGCTCTTCTGTGGTGGGTGTGAGCTTGCAGCATTTGCCGAAAGTCCGCCAGGCGAAG 1522
DB 543 AAAGAGAGAACTCTTCTGTGTTGTTTATCTGTTGACAGAGAGCTTCTGTCAGCAAA 601

QY 1523 CAGAGTTCCTCGCGCGCTCAGCAAGTTTATTCGCGCTTACTTGTGATTTATTCCTGCGAG 1582
DB 1523 CAGAGTTCCTCGCGCGCTCAGCAAGTTTATTCGCGCTTACTTGTGATTTATTCCTGCGAG

```

```

Db 602 -AGCAGATTCAATGACCTCTGCAAGTTCAATGAGTCTACTTGTGATCTCTGAG 660
QY 1583 GGAGACGTCCTCCGCGTCTCTAGACCTGAGTACCAA 1617
DB 661 GGAGACATCTCTGCTATCTGATCTAAGTACCAA 695

RESULT 13
BY726061 667 bp mRNA linear EST 17-DEC-2002
LOCUS clone B020034F22 5', mRNA sequence.
DEFINITION BY726061.1 GI:27139188
ACCESSION BY726061
VERSION Mus musculus (house mouse)
KEYWORDS EST.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 667)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bratt, D., Brusic, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayata, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suihito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

```

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers

1..667

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="B020034F22"

/tissue_type="egg"

/dev_stages="2 cells"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, 2 cells egg"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."

ORIGIN

Query Match 17.5%; Score 416; DB 6; Length 667;

Best Local Similarity 87.8%; Pred. No. 1.3e-104;

Matches 452; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 252 AGGAGTGGGCGCAGCAGCAAGACAGTGGGCTGTACAAATCACCTTCAATATGACA 311

Db 153 AGGGAGTGGGCGCGCAGCAGCAAGACAGCGGACTGCACAACATCACCTTCAGATACGACA 212

Qy 312 ATTGTACCACCTACTTGAATCCAGTGGGGAAGCATGTGATTGCTGACGCCAGAAATCA 371

Db 213 ACTGTACCACCTACTTGAATCCGGCGGAAGCATGCGATTGCTGATCTCAGAACATCA 272

Qy 372 CCATCAGCCAGTATGCTTGGCCATGACCAAGTGGCAGTCACCATCTTTTGGTCCCCAGGG 431

Db 273 CCATCAGCCAGTACGCTTGGCCACGCGAGGTGGCAGTCACCATCTTTTGGTCCCCAGGG 332

Qy 432 CCCTCGGCATCGAATCTCTGAAGATTTCCGGTAACTACTGGAGAGCTGAAGTCGGAGG 491

Db 333 CCCTTGGCATTGAATTTCTTAAAGGATTTCCGAGTCATCTCGAGAGCTGAAGTCGGAGG 392

Qy 492 GAAGACGTGCCAACAACTGATCTTAAAGGATCCGAAGCATCGAAGCTCAACAGTAGCTTCAAAA 551

Db 393 GCAGACGTGCCAACAGCTGATTTCTTAAAGGACCCCAACAGCTCAACAGCAGCTTCAGAA 452

Qy 552 GAATCGGAATGGAATCTCAACCTTTTCCCTGAATATGAATTTTGAACAGGATTTATTTCTGTA 611

Db 453 GGACTGGAATGGAATCTCAGCTTTTCTGTAATATGAATTTTGAACAGGATTTATTTCTGTA 512

Qy 612 AGTTGTCCCTTTTCTTCCATTAATAAAGCAAGCAATACACCTTTCTTCTTTAGAA 671

Db 513 AGATTGTCCCTTTTCTTCCATTAATAAAGCAATTAACATCCCTTTCTTCTTTAGAA 572

Qy 672 CCCGAGCCTGTGACCTGTGTTTACAGCGCGCAACTCTAGCTTGTGTAACCCCTTCTTCTGGAAGC 731

Db 573 CACGGGCTGTGACCTGTGTGTACCACTGGCTGTAGCTTCTTCTGGAAGC 632

Qy 732 CTGGAACCTGAACATCAGCAGCATGCTCGGAC 766

Db 633 CTCGGAACCTGAATATCAGCAGCATGCTTCTGAC 667

RESULT 14

BQ830554 548 bp mRNA linear EST 15-SEP-2002

LOCUS L61n20509 AFT024-subtracted library Mus musculus cDNA 5' similar to Hypothetical human protein DKFZp434N1928, mRNA sequence.

DEFINITION BQ830554

ACCESSION BQ830554

VERSION BQ830554.1 GI:22862622

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 548)

AUTHORS Hackney, J.A., Charbord, P., Brunk, B.P., Stoeckert, C.J., Lemischka, I.R. and Moore, K.A.

TITLE A molecular profile of a hematopoietic stem cell niche

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 13061-13066 (2002)

MEDLINE 22247628

PUBMED 12226475

COMMENT Contact: Moore, Kateri A.

Department of Molecular Biology

Princeton University

217 Lewis Thomas Laboratory, Washington Road, Princeton, NJ 08544, USA

Tel: 609 258 0605

Fax: 609 258 2759

Email: kmoores@molbio.princeton.edu

These ESTs are derived from a subtracted cDNA library enriched for gene products expressed by a hematopoietic stem cell-supporting stromal cell line, AFT024.

Seq primer: M13Reverse or T7.

FEATURES

source

1..548

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/tissue_type="Fetal Liver"

/cell_type="Stromal cell"

/cell_line="AFT024"

/dev_stage="Embryonic day 14-14.5"

/lab_host="DH10B"

/clone_lib="AFT024-subtracted library"

/note="Organ: Fetal Liver; Vector: Sport 1; Site 1: Sal I; Site 2: Not I; Two directionally cloned cDNA libraries were made from a hematopoietic stem cell-supporting stromal cell line (AFT024) and from a non-supporting stromal cell line (2018). Subtractive hybridization was performed by hybridization of the target, AFT024, single stranded cDNA library in pSport1 to biotinylated RNA transcribed from the driver, 2018 cDNA library in pSport2 with inserts cloned in the complementary orientation. The AFT024-subtracted library contains 4.2x105 clones and is depleted of common housekeeping gene products eg. beta-actin and enriched for transcripts specific to AFT024. For detailed protocols and additional information please see our website at <http://stromalcell.princeton.edu>."

ORIGIN

Query Match 17.4%; Score 414.4; DB 5; Length 548;

Best Local Similarity 85.1%; Pred. No. 3.3e-104;

Matches 463; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 527 AAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTCTCTGTAATATG 586


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Db 2 AAACAGCTCAACAGCAGCTTTCAGAGGACTGGAATGGAATCTCAGCCTTTCCTGAATATG 61
Qy 587 AATTTTGAACGGATTATTTGTAAGGTTGTCCTTTTCTCCATTAATAAAGCAGC 646
Db 62 AATTTGAGACGGATTACTTTTGAAGATGTCCCTTTCCCTTCATTAATAAAGCAGC 121
Qy 647 AATTACCACTTCTTCTTTAGAACCCGAGCTGTGACCTGTGTTGTATACAGCCGACAAAT 706
Db 122 AATTACCACTTCTTCTTTAGAACCCGAGCTGTGACCTGTGTTGTATACACCTGACAAAC 181
Qy 707 CTAGCTTTGAACCCCTTCTGGAAGCTTGGAACTCTGGAACATCAGCCAGCATGGCTCGGAC 766
Db 182 TTGGCTGTGAAGCTTTCTGGAAGCTTGGAACTCTGGAACATCAGCCAGCATGGTTCTGAC 241
Qy 767 ATGCAAGTGTCTTGCACATGACCCGACACACTTCCGCTTCCGTTTCTTCTTCTTCTAC 826
Db 242 ATGCAAGTGTCTTGCACATGACCCGACACACTTCCGCTTCCGTTTCTTCTTCTTCTC 301
Qy 827 TACAGCTCAAGCAGGAGGACCTTTCAAGCGAAGACCTGTAAGCAGGAGCAGCAACTACA 886
Db 302 TATAGCTCAAGCAGGAGGACCTTTCAAGCGAAGACCTGTAAGCAGGAGCAGCAACTACA 361
Qy 887 GAGACGACCTGCTCTCTTCAAAATGTTTCTCCAGGGGATTAATTAATTCAGCTGCTG 946
Db 362 GAGACGACCTGCTCTCTTCAAAATGTTTCTCCAGGGGATTAATTAATTCAGCTGCTG 421
Qy 947 GATGACACTAACACAAAGAAAGTGTATGATTAATGCTTAAAGCAGTGCACCTCCCG 1006
Db 422 GATGACAGCAACACCAAGGAAAGCTGCTCAGTATGTGGTGAAGTCAAGTGCAGTCTCCC 481
Qy 1007 TGGGCGGCGCCATCAGAGCGCTGCGCCATCAGTGCCACTGTAGTCAATATCGGCATTC 1066
Db 482 TGGGCTGGAAGCCATCAGAGCTGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
Qy 1067 GCGA 1070
Db 542 GCAA 545

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RESULT 15

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BX750910/c
LOCUS BX750910 886 bp mRNA linear EST 09-DEC-2003
DEFINITION BX750910 XGC-gastrula Xenopus tropicalis cDNA clone TGAs082k14 3',
mRNA sequence.

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ACCESSION BX750910
VERSION BX750910.1 GI:39640978

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KEYWORDS EST.

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SOURCE Xenopus tropicalis (western clawed frog)

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ORGANISM Xenopus tropicalis

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

```

```

REFERENCE 1 (bases 1 to 886)

```

```

AUTHORS Croning M.D.R., Ashurst J.L., Taylor R., Zorn A.M. and Rogers J.

```

```

TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)

```

```

JOURNAL Unpublished (2003)

```

```

COMMENT Contact: Croning MDR

```

```

Sanger Institute

```

```

Hinxton, Cambridgeshire, CB10 1SA, UK

```

```

Email: trop@sanger.ac.uk

```

```

Sanger Xenopus tropicalis EST project 2001

```

```

TROPICALIS_SEQUENCE_ID: TGAs082k14.q1kT7

```

```

Sequencing primer: T7

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This sequence is from a Xenopus Gene Collection (XGC) library

```

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constructed by Aaron M. Zorn.

```

```

cDNA was oligo dT primed from Sug of poly A+ RNA from stages 10-13

```

```

gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with

```

```

EcoRI at the 5' end and NotI at the 3' end.

```

```

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

```

```

Host: Escherichia coli XL1-blue.

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FEATURES

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Location/Qualifiers

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1..886

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```

source

```

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/mol_type="mRNA"
/db_xref="taxon:8364"
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/lab_hosts="Escherichia coli XL1-blue"
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/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."

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ORIGIN

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Query Match 17.3%; Score 411.6; DB 5; Length 886;
Best Local Similarity 67.5%; Pred. No. 2.4e-103;
Matches 598; Conservative 0; Mismatches 279; Indels 9; Gaps 1;
Qy 1067 GCGACGCTTTCTACCTGTGATGTGCGCAAGCAACAAAGAAATATATATTCACATTTA 1126
Db 886 GCCACTCTATTCTACTGTAAATGTGCGCAAGCAAGCAAGAAACATTTACTCACCCTG 827
Qy 1127 GATGAAGAGAGCTCTGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGGCTCCGG 1186
Db 826 GACGAGGAGAGTTCGGAATCTTCTACTTACGCGGAGTCTGCATGTGGAGAAACCGCGT 767
Qy 1187 CCGCGCGCGAAGGTCTTTCTCTGCTATTCTCAAGTAAAGATGCGCAAAATCAATGAATGTC 1246
Db 766 CCGCGCGCTCGAGTTTATTGTTCTCTAGTAAAGACTGTCAAAGACACATTAATGTC 707
Qy 1247 GTCCAGTGTTCGCTTACTTCTCCAGGACTTCTGTGGCTGTGAGTGGCTCTTGACCTG 1306
Db 706 ATCCAGTGTTCGCTTACTTCTCAAGATTTCTGTGGTGTGAGTTCGTGACCTG 647
Qy 1307 TGGGAAGACTTCAGCTCTGTAGAGAGGGCAGAGAGATGGTTCATCCAGAGATCCAC 1366
Db 646 TGGGAAGACTTGAAGATCTGCAAGAGCGGCGAGTGGCTGGAACAAAGATCCGG 587
Qy 1367 GAGTCCCAAGTTCATCATTTGTTGTTTCCAAAGTATGAAGTACTTTGTGGACAAGAAG 1426
Db 586 GATTCCCACTACATCATCTGCTGCTCAGAGGCTCAAGTACTTTGTGGAGAGAG 527
Qy 1427 AACTACAACAAAGAGGAGTGGCGGAGCTCGGGGAAAGAGAGCTCTTCTGTTGGGG 1486
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Db 406 GAGCTTGGGAATTCATCACCCTTATTTTCAATTTCTTCTCGACTCGGACATCCCGGA 347
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Db 346 ATCTTGGACACACCAAGAGTACAACTGATGGACCACTTCCCGAGCTCTTACTACCAC 287
Qy 1658 TTGCACTCCCGAGACCAAGGCTTCAGAGCGCGGGGAGCAGCACCGGACAGGGGAGCAGA 1717
Db 286 CTGTACTCCAAGGAGCTGAGCTGGCAGCACCGGAGAGTACCCCGCCCAACATCAGCAAG 227
Qy 1718 AGGACTACTTCCGAGCAAGTTCAGGCGGCTCCCTATAGCTCGCCATTTGCAACATGAC 1777
Db 226 CGCAACTACTTCCGAGCAAGCGCGGCTCGCTCTACATCGCCATCTGCAACATGAC 167
Qy 1778 CAGTTTATGACGAGGAGCGGCTGTTTCGAAAGACAGTTCGTTCCCTTCATCTCTCT 1837
Db 166 CAGTACCAAGGAGCAAGCGGCTGTTTCGAGAGAGCAGCACTCCCGGCCCACTCCCG 107
Qy 1838 CCATGCGCTACCGGAGCAGTCTTGGAGAAATTTGATTCGGGCTTGGTTTAAATGAT 1897
Db 106 ACCCTCCACTACGAGGAGCGGCTCATGGAGAGTTTCGACTCCGGGTGGTGTGTAACGAC 47

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 03:35:56 ; Search time 1906 Seconds

(without alignments)
3787.947 Million cell updates/sec

Title: US-10-717-282-1_COPY_86_234

Perfect score: 149

Sequence: 1 atggccgctggtcagct.....aaagcgtgcccgcaccgcg 149

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 149 | 100.0 | 2383 | 6 | AX364570 Sequence |
| 2 | 149 | 100.0 | 2383 | 6 | AX364573 Sequence |
| 3 | 127 | 85.2 | 2341 | 6 | AX364576 Sequence |
| 4 | 127 | 85.2 | 2724 | 9 | AF458067 Homo sapi |
| 5 | 127 | 85.2 | 4392 | 6 | AX392973 Sequence |
| 6 | 127 | 85.2 | 4477 | 9 | AF494208 Homo sapi |
| 7 | 126.8 | 85.1 | 154606 | 9 | AC097358 Homo sapi |
| 8 | 125.4 | 84.2 | 2037 | 9 | AB093642 Macaca fa |
| 9 | 123.8 | 83.1 | 3083 | 6 | AX351723 Sequence |
| 10 | 122.4 | 82.1 | 2786 | 6 | AX350979 Sequence |
| 11 | 112.6 | 75.6 | 2203 | 10 | BC066804 Mus muscu |
| 12 | 112.6 | 75.6 | 2387 | 10 | AF494210 Mus muscu |
| 13 | 112.6 | 75.6 | 2443 | 6 | AX364580 Sequence |
| 14 | 112.6 | 75.6 | 3366 | 10 | AF459444 Mus muscu |
| 15 | 112.4 | 75.4 | 134122 | 10 | AC125152 Mus muscu |
| 16 | 112.4 | 75.4 | 179891 | 2 | AC124603 Rattus no |
| 17 | 110.8 | 74.4 | 258797 | 2 | AC116282 Rattus no |
| 18 | 110.8 | 74.4 | 295304 | 2 | AC119550 Rattus no |
| 19 | 104.6 | 70.2 | 2259 | 6 | AX364572 Sequence |

| | | | | | | |
|------|-------|------|--------|---|-------------|--------------------|
| 20 | 104.6 | 70.2 | 2259 | 6 | AX364575 | Sequence |
| 21 | 88.8 | 59.6 | 2217 | 6 | AX364578 | Sequence |
| 22 | 87.8 | 58.9 | 2217 | 6 | AX364582 | Sequence |
| 23 | 83.6 | 56.1 | 2214 | 6 | AX350981 | Sequence |
| 24 | 51.6 | 34.6 | 2566 | 5 | AY278204 | Gallus ga |
| 25 | 41.6 | 27.9 | 18876 | 6 | AX803758 | Sequence |
| 26 | 41.6 | 27.9 | 61944 | 6 | AX803750 | Sequence |
| C 27 | 40 | 26.8 | 110000 | 1 | AP006840_25 | Continuation (26 o |
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| C 36 | 38 | 25.5 | 2196 | 9 | HUMPRKCI | Human prote |
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| C 38 | 38 | 25.5 | 2320 | 9 | BC022016 | Homo sapi |
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| C 43 | 38 | 25.5 | 157662 | 8 | AC120538 | Oryza sat |
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ALIGNMENTS

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| LOCUS | AX364570 | | | | | |
| DEFINITION | AX364570 | | | | | |
| ACCESSION | AX364570 | | | | | |
| VERSION | AX364570.1 | GI:18696530 | | | | |
| KEYWORDS | | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | 1 | | | | | |
| AUTHORS | Presnell,S.R., Kuestner,R.E. and Gao,Z. | | | | | |
| TITLE | Human cytokine receptor | | | | | |
| JOURNAL | Patent: WO 0208259-A 1 31-JAN-2002; | | | | | |
| FEATURES | ZymoGenetics, Inc. (US) | | | | | |
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| | GATGPADSQHSQHGGLDQGEARPDALGSAALQPLHTVKAGSPDMPRDSITDSS | | | | | |
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ORIGIN

Query Match 100.0%; Score 149; DB 6; Length 2383;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 60
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DB 206 TGGAGGATGAAGCGGCTGCCCGACCCCG 234
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DEFINITION Sequence 4 from Patent WO0208259.
ACCESSION AX364573
VERSION AX364573.1 GI:18696533
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Prenell, S.R., Kuestner, R.E. and Gao, Z.
Human cytokine receptor
Patent: WO 0208259-A 4 31-JAN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 149; DB 6; Length 2383;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 60
|||||
DB 86 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 145
|||||

QY 61 TCGAGCTGGCTGTGGCGCTGGCGGCTCCGGCCGCGCGGGCGCGACACCTGTGGC 120
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DB 146 TCGAGCTGGCTGTGGCGCTGGCGGCTCCGGCCGCGCGGGCGCGACACCTGTGGC 205
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QY 121 TGGAGGATGAAGCGGCTGCCCGACCCCG 149
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ORIGIN

Query Match 100.0%; Score 149; DB 6; Length 2383;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 60
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QY 121 TGGAGGATGAAGCGGCTGCCCGACCCCG 149
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Db 206 TGGAGGATGAAGCGGCTGCCCGACCCCG 234
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RESULT 3
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LOCUS AX364576 2341 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 7 from Patent WO0208259.
ACCESSION AX364576
VERSION AX364576.1 GI:18696536
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Prenell, S.R., Kuestner, R.E. and Gao, Z.
Human cytokine receptor
Patent: WO 0208259-A 7 31-JAN-2002;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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ORIGIN

Query Match 85.2%; Score 127; DB 6; Length 2341;
Best Local Similarity 93.0%; Pred. No. 6.3e-16;
Matches 133; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 86 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 145
|||||

QY 61 TCGAGCTGGCTGTGGCGCTGGCGGCTCCGGCCGCGCGGGCGCGACACCTGTGGC 120
|||||

DB 146 TCGAGCTGGCTGTGGCGCTGGCGGCTCCGGCCGCGCGGGCGCGACACCTGTGGC 205
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QY 121 TGGAGGATGAAGCGGCTGCCCG 143
|||||

DB 206 TGGAGGAGTGGGGCCAGCCAG 228
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RESULT 4
AF458067
LOCUS AF458067 2724 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens IL-17RD mRNA, complete cds.
ACCESSION AF458067
VERSION AF458067.1 GI:21779862
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2724)


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ORIGIN

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ACCESSION AC097358
VERSION AC097358.2 GI:21166205
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
Haugen, E.D.
Direct Submission
Unpublished
2 (bases 1 to 154606)
Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
Submitted (16-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 154606)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
Saenphimmachak, C., Phelps, K.A., Buckley, D., Raymond, C. and
Haugen, E.D.
Direct Submission
Submitted (24-MAY-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On May 24, 2002 this sequence version replaced gi:16152308.
----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
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Web site: http://www.genome.washington.edu
Contact: uwchgts@u.washington.edu
----- Project Information
Center project name: chr-3
Center clone name: RP11-157F20 (bc0274)
----- Summary Statistics
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET; 96% of reads
Chemistry: Dye-terminator Big Dye; 4% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 154096 bases at least Q40
Consensus quality: 154548 bases at least Q30
Consensus quality: 154600 bases at least Q20
Insert size: 154606; sum-of-contigs
Quality coverage: 8.5x in Q20 bases; sum-of-contigs
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Overlapping Sequences:
5': RP11-263116 (UWGC:bc0327) AC092050, 123826-bp overlap
3': RP11-241K3 (UWGC:bc0319) AC093928
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.
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Sequence Validation:
This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.
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exclude fragments <1.5kb. The SfilI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method. Custom primers used for sequencing (5' end primer [CTTCTGCTCTAAAGCTGG] ; 3' end primer [CCACTGCAGCTCGAGCACA]).

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Db 91 TCGAGCTAGCTGTGGCGCTGGCGGTCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCG 150
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ORIGIN

Query Match 84.2%; Score 125.4; DB 9; Length 2037;
Best Local Similarity 92.3%; Pred. No. 1.3e-15;
Matches 132; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ATGGCCCCGTGCTGCAGCTCTGCTCCGCTCTTTTACGCTCAACGCTGCTCAACGCG 60
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Db 91 TCGAGCTAGCTGTGGCGCTGGCGGTCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCG 150
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FEATURES

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FEATURES

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ORIGIN

Query Match 83.1%; Score 123.8; DB 6; Length 3083;
Best Local Similarity 91.6%; Pred. No. 2.6e-15;
Matches 131; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ATGGCCCCGTGCTGCAGCTCTGCTCCGCTCTTTTACGCTCAACGCTGCTCAACGCG 60
Db 22 ATGGCCCCGTGCTGCAGCTCTGCTCCGCTCTTTTACGCTCAACGCTGCTCAACGCG 81
Qy 61 TCGAGCTGGCTGTGGCGCTGGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 82 TCGAGCTGGCTGTGGCGGTCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 141
Qy 121 TGGAGGATGAAGCGGCTGCCCG 143
Db 142 TGGAGGGAGTAGGCGCGCCAG 164

RESULT 10

AX350979
LOCUS AX350979 2786 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 13 from Patent WO0190358.
ACCESSION AX350979
VERSION AX350979.1 GI:18616355
KEYWORDS .
SOURCE unidentified
ORGANISM unclassified.

REFERENCE

1
Gorman, D.M.
Mammalian receptor proteins; related reagents and methods
Patent: WO 0190358-A 13 29-NOV-2001;
SCHERING CORPORATION (US)

FEATURES

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/note="unnamed protein product"

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ESESSESTYTAALPRELRPRPKVFLCYSKDQGNHNVQCFAYFLQDFGCGEVALD
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FHPPLRYREPVLEKFDGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHESQH
GLDDGEARPALDGSAAQLPLLHTVKAGSPDMPRDSGIYDSSVPSELSLPLMEGLS
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118..2283
/product="unnamed"

ORIGIN

Query Match 82.1%; Score 122.4; DB 6; Length 2786;
Best Local Similarity 90.2%; Pred. No. 5.1e-15;

| Matches | 129; | Conservative | 0; | Mismatches | 14; | Indels | 0; | Gaps | 0; |
|---------|------|---|-----|------------|-----|--------|----|------|----|
| y | 1 | ATGGCCCCGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCCTGCTCAACGGC | 60 | | | | | | |
| b | 70 | ATGGCCCCGCTGCAGCTCTGCTCCGCTCTTTACGGTCAACGCCTGCTCAACGGC | 129 | | | | | | |
| y | 61 | TCGCAGCTGGCTGTGGCCGCTGGGGGCTCCGGCCGCGCGGGGGCGCCGACCTGTGGC | 120 | | | | | | |
| b | 130 | TCGCAGCTGGCTGTGGCCGCTGGGGGCTCCGGCCGCGCGGGGGCGCCGACCTGTAGC | 189 | | | | | | |
| y | 121 | TGGAGGATGAAGCGGCTGCCCG | 143 | | | | | | |
| | 190 | TGGANGGGAGTGGGCCAGCCAG | 212 | | | | | | |

| |
|--|
| RESULT 11 |
| BC066804 |
| OCUS |
| BC066804 |
| Mus musculus cDNA clone IMAGE:30091051, partial cds. |
| BC066804 |
| mRNA linear ROD 05-MAR-2004 |
| 2203 bp |
| GI:45219858 |
| BC066804.1 |
| SEQUENCE |

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2203)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D.,
Altchul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Pahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

| | | | | | |
|-----------|--|--|------|-------------|--------|
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. | 99 | (26) | 16899-16903 | (2002) |
| PUBMED | 12477932 | | | | |
| REFERENCE | 2 | (bases 1 to 2203) | | | |
| AUTHORS | Strausberg, R. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (01-MAR-2004) | National Institutes of Health, Mammalian | | | |
| | Gene Collection (MGC), Cancer Genomics Office, National Cancer | | | | |
| | Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, | | | | |
| | USA | | | | |
| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov | | | | |

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Angelo L. Vescovi (Institute fro Stem Cell
Research, Italy)
cDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: <http://agsun.grc.nia.nih.gov/cDNA/>)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-sbgs.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grinwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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Series: IRAX Plate: 144 Row: e Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 24025661.

FEATURES
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            /strain="CD1"
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ORIGIN

[illegible]

RESULT 12

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| AF494210 | AF494210 | 2387 bp | linear | ROD 08-DEC-2003 |
| LOCUS | Mus musculus strain BALB/c | Interleukin 17 receptor-like protein long form (Il17rlm) mRNA, complete cds; alternatively spliced. | | |
| DEFINITION | AF494210 | | | |
| ACCESSION | AF494210.1 | GI:21667507 | | |
| VERSION | | | | |
| KEYWORDS | Mus musculus (house mouse) | | | |
| SOURCE | Mus musculus | | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; | | | |
| REFERENCE | 1 (bases 1 to 2387) | | | |
| AUTHORS | Xiong,S., Zhao,Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S., Liu, L., and Chang, Z. | | | |
| TITLE | Hsf1 Inhibits PC-12 Cell Differentiation by Interfering with Ras-Mitogen-activated Protein Kinase MAPK Signaling | | | |
| JOURNAL | J. Biol. Chem. | 278 (50), 50273-50282 | (2003) | |
| PUBMED | 12958313 | | | |
| REFERENCE | 2 (bases 1 to 2387) | | | |
| AUTHORS | Xiong,S.Q., Huang,G.R., Zhao,Q.H., Chen,P.L., Rong,Z.L., Ye,X.Y., Chen,Y., Liu,L., Fu,X.Y. and Chang,Z.J. | | | |
| TITLE | Direct Submission | | | |
| JOURNAL | Submitted (22-WAR-2002) Tsinghua Institute of Genome Research, | | | |

FEATURES

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1. .2387
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164. .2380
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ORIGIN

Query Match 75.6%; Score 112.6; DB 10; Length 2387;
Best Local Similarity 86.7%; Pred. No. 4.7e-13;
Matches 124; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ATGGCCCGTGGCTGCAGCTCTGCTCCGCTCTCTTTACGGTCAACGCCCTGCTCAACGCC 60
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Qy 61 TCGCAGCTGGCTGTGGCGGCTCGCGGGTCCGGCGCGCGCGCGCGCGACACCTGTGGC 120
Db 224 TCGCAGCTGGCAGTGGCGCGGCGGCTCGCGCGCGCGCGCGCGCGACACCTGTGGC 283

Qy 121 TGGAGGATGAAGCGCGCTGCCCG 143
Db 284 TGGAGGAGTGGGGCGGCCAG 306

RESULT 13
AX364580
LOCUS AX364580 2443 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 11 from Patent WO0208259.
ACCESSION AX364580
VERSION AX364580.1 GI:18696539
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Preenell, S.R., Kuestner, R.E. and Gao, Z.
Human cytokine receptor
Patent: WO 0208259-A 11 31-JAN-2002;
ZymoGenetics, Inc. (US)

FEATURES
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101..2320
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ORIGIN

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Matches 124; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy 61 TCGCAGCTGGCTGTGGCGGCTCGCGGGTCCGGCGCGCGCGCGCGACACCTGTGGC 120
Db 161 TCGCAGCTGGCAGTGGCGCGGCGGCTCGCGCGCGCGCGCGCGACACCTGTGGC 220

Qy 121 TGGAGGATGAAGCGCGCTGCCCG 143
Db 221 TGGAGGAGTGGGGCGGCCAG 243

RESULT 14
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LOCUS AF459444 3366 bp mRNA linear ROD 15-MAY-2002
DEFINITION Mus musculus transmembrane protein (Sef) mRNA, complete cds.
ACCESSION AF459444
VERSION AF459444.1 GI:20799327
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Lin, W., Furthauer, M., Thiese, B., Thiese, C., Jing, N. and Ang, S.L.
Cloning of the mouse Sef gene and comparative analysis of its
expression with Fgf8 and Spry2 during embryogenesis
Mech. Dev. 113 (2), 163-168 (2002)
JOURNAL MECH. DEV. 113 (2), 163-168 (2002)
MEDLINE 21959295
PUBMED 11960706
REFERENCE 2 (bases 1 to 3366)
AUTHORS Lin, W. and Ang, S.-L.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-2001) I.G.B.M.C., 1, rue Laurent Fries, Iilkirch
67404, France

FEATURES
Location/Qualifiers
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| Query Match | 75.4%; Score 112.4; DB 10; Length 134122; |
| Best Local Similarity | 91.5%; Pred. No. 2.8e-13; |
| Matches 119; Conservative 0; Mismatches 11; Indels 0; Gaps 0; | |
| Qy | 1 ATGGCCCGTGGGTGAGCTCTGCCTTCCTTTACGGTCAACGCCCTGCTCAACGGC 60 Db |
| 29380 | ATGGCCCGTGGGTGAGCTCTGCCTTCCTTTACTGTCAACGCCCTGTCTCAACGGC 29439 |
| Qy | 61 TCGCACGTCGCTTGCGCCCTCGCGGCTCGCGCCGCGCGGGGCGCGACA CTTGTGGC 120 |
| Db | 29440 TCGCACGTCGCTTGCGCCCTCGCGGCTCGCGCCGCGAGGGGCGCGA CACTGTGGC 29499 |
| Qy | 121 TGGAGGATGA 130 |
| Db | 29500 TGGAGGATA 29509 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---------------|------------------|------------|------------------|------------|------------------|------------|------------------|------------|-------------------|------------|-------------------|------------|------------------|------------|-------------------|------------|------------------|------------|------------------|------------|-------------------|------------|-------------------|------------|------------------|------------|------------------|------------|------------------|------------|-------------------|------------|-------------------|------------|------------------|------------|------------------|------------|------------------|-------------|------------------|--------------|------------------|--------------|----------------------|--------------|--------------------|--------------|------------------|--------------|------------------|--------------|------------------|--------------|-------------------|--------------|------------------|--------------|---------------------|--|--------------|-------------------|--------------|------------------|--------------|-------------------|--------------|------------------|--------------|-------------------|--------------|------------------|
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2005, 03:30:47 ; Search time 432 Seconds
(without alignments)
2041.763 Million cell updates/sec

Title: US-10-717-282-1_COPY_86_234

Perfect score: 149

Sequence: 1 atggcccgctggtgcagct.....aaagcggtgcccgaccgccg 149

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----|--------------------|
| 1 | 149 | 100.0 | 2383 | 6 | ABA95031 Human cyt |
| 2 | 149 | 100.0 | 2383 | 6 | ABA95033 Human cyt |
| 3 | 127 | 85.2 | 2341 | 6 | ABA95035 Human cyt |
| 4 | 127 | 85.2 | 4392 | 6 | ABK62082 Human cdn |
| 5 | 123.8 | 83.1 | 3083 | 4 | AAS15346 DNA encod |
| 6 | 122.4 | 82.1 | 2786 | 6 | AAS18134 Human DNA |
| 7 | 112.6 | 75.6 | 2443 | 6 | ABA95037 Murine cy |
| 8 | 104.6 | 70.2 | 2259 | 6 | ABA95034 Human cyt |
| 9 | 104.6 | 70.2 | 2259 | 6 | ABA95032 Human cyt |
| 10 | 88.8 | 59.6 | 2217 | 6 | ABA95036 Human Zcy |
| 11 | 87.8 | 58.9 | 2217 | 6 | ABA95038 Murine cy |
| 12 | 83.6 | 56.1 | 2214 | 6 | AAS18135 Human DCR |
| 13 | 41.6 | 27.9 | 18876 | 10 | ADI23928 Streptomy |
| 14 | 41.6 | 27.9 | 61944 | 8 | ADI23920 Streptomy |
| 15 | 38.4 | 25.8 | 567 | 8 | ACA26238 Prokaryot |
| 16 | 38 | 25.5 | 1407 | 12 | ADM94405 Rice brit |
| 17 | 38 | 25.5 | 2196 | 2 | AAQ71197 Human pro |
| 18 | 38 | 25.5 | 2196 | 3 | AAA35296 Human ade |
| 19 | 38 | 25.5 | 2196 | 3 | AAF21418 Human low |
| 20 | 38 | 25.5 | 2196 | 10 | ABZ97112 Human nuc |

| | | | | | |
|------|------|------|-------|----|----------|
| c 21 | 38 | 25.5 | 2196 | 11 | ABD20961 |
| c 22 | 38 | 25.5 | 2196 | 12 | ADI81649 |
| c 23 | 38 | 25.5 | 38644 | 3 | AAA35302 |
| c 24 | 38 | 25.5 | 38644 | 3 | AAF21424 |
| c 25 | 38 | 25.5 | 38644 | 10 | ABZ97118 |
| c 26 | 38 | 25.5 | 38644 | 11 | ABD20967 |
| c 27 | 38 | 25.5 | 80928 | 12 | ADO25290 |
| c 28 | 36 | 24.2 | 1671 | 4 | ABL09901 |
| c 29 | 36 | 24.2 | 1671 | 4 | ABL09900 |
| c 30 | 35.6 | 23.9 | 1620 | 4 | AAS51502 |
| c 31 | 35.6 | 23.9 | 1620 | 8 | ACA19515 |
| c 32 | 35.6 | 23.9 | 1674 | 11 | ABD03041 |
| c 33 | 35.6 | 23.9 | 1785 | 11 | ABD02924 |
| c 34 | 35.2 | 23.6 | 2757 | 8 | ACA25644 |
| c 35 | 35.2 | 23.6 | 4010 | 4 | AAS11603 |
| c 36 | 34.8 | 23.4 | 17955 | 2 | AAV56642 |
| c 37 | 34.6 | 23.2 | 474 | 9 | ACH14819 |
| c 38 | 34.6 | 23.2 | 1367 | 4 | AAD16506 |
| c 39 | 34.6 | 23.2 | 1367 | 5 | AAS29733 |
| c 40 | 34.6 | 23.2 | 1367 | 9 | ADA27261 |
| c 41 | 34.6 | 23.2 | 1367 | 10 | ADA12864 |
| c 42 | 34.6 | 23.2 | 1437 | 5 | AAS29631 |
| c 43 | 34.6 | 23.2 | 2383 | 4 | AAH18672 |
| c 44 | 34.6 | 23.2 | 2392 | 11 | ADM01573 |
| c 45 | 34.6 | 23.2 | 2487 | 4 | AAH14983 |

ALIGNMENTS

RESULT 1

ABA95031

ID ABA95031 standard; DNA; 2383 BP.

AC ABA95031;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 nucleotide sequence.

KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
pulmonary alveolar proteinosis; familial periodic fever; antitumor;
erythroleukemia; chromosome 3p14.3; gene therapy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 86..2347

FT /*tag= a

FT /product= "Zcytor18"

PN WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX P-PSDB; ABB07626.

XX New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor growth,
and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 5; Page 85-90; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide

CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumour growth. The
 CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
 CC and localize Zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human Zcytor18 nucleotide sequence

SQ Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;
 Query Match 100.0%; Score 149; DB 6; Length 2383;
 Best Local Similarity 100.0%; Pred. No. 1e-26;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGCTGCTCAACCGC 60
 DB 86 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGCTGCTCAACCGC 145
 QY 61 TCGCAGCTGGCTGTGGCGCTGGCGGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 146 TCGCAGCTGGCTGTGGCGCTGGCGGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
 QY 121 TGGAGGATGAAAGCGGCTGCCCGACCCCG 149
 DB 206 TGGAGGATGAAAGCGGCTGCCCGACCCCG 234

RESULT 2
 ABA95033
 ID ABA95033 standard; DNA; 2383 BP.

AC ABA95033;

DT 20-MAY-2002 (first entry)

XX Human cytokine receptor, Zcytor18 variant nucleotide sequence.

XX Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 86..2347
 FT /*tag= a
 FT /product= "Zcytor18 variant"

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX P-PSDB; ABB07627.

XX New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.

PS Disclosure; Page 94-98; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide
 CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumour growth. The
 CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
 CC and localize Zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human Zcytor18 variant nucleotide sequence

SQ Sequence 2383 BP; 558 A; 681 C; 638 G; 506 T; 0 U; 0 Other;

Query Match 100.0%; Score 149; DB 6; Length 2383;
 Best Local Similarity 100.0%; Pred. No. 1e-26;
 Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGCTGCTCAACCGC 60

DB 86 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTCTTTACGGTCAACGCTGCTCAACCGC 145

QY 61 TCGCAGCTGGCTGTGGCGCTGGCGGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120

DB 146 TCGCAGCTGGCTGTGGCGCTGGCGGTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205

QY 121 TGGAGGATGAAAGCGGCTGCCCGACCCCG 149

DB 206 TGGAGGATGAAAGCGGCTGCCCGACCCCG 234

RESULT 3

ABA95035

ID ABA95035 standard; DNA; 2341 BP.

AC ABA95035;

DT 20-MAY-2002 (first entry)

XX Human cytokine receptor, Zcytor18 splice variant nucleotide sequence.

XX Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 86..2305
 FT /*tag= a
 FT /product= "Zcytor18 splice variant"

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX P-PSDB; ABB07628.

XX New cytokine receptor polypeptide designated zcytor18, useful for


```

QY 121 TCGAGGATGAAGCGGCTGCCGACCCG 149
DB 121 TCGMGATGAARGCNGCNGCNGCNGCNG 149

RESULT 9
ABA95032
ID ABA95032 standard; DNA; 2259 BP.
AC ABA95032;
XX
XX
XX 20-MAY-2002 (first entry)
XX
XX Human cytokine receptor, Zcytor18 degenerate coding sequence.
DE
XX Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX WO200208259-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US023253.
XX
XX 26-JUL-2000; 2000US-0220747P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Presnell SR, Kuestner RE, Gao Z;
PI
XX WPI; 2002-217048/27.
XX
XX P-PSDB; ABB07626.
XX
XX New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX
XX Disclosure; Page 92-93; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumour growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 degenerate coding sequence
XX
SQ Sequence 2259 BP; 379 A; 234 C; 373 G; 293 T; 0 U; 980 Other;

Query Match 70.2%; Score 104.6; DB 6; Length 2259;
Best Local Similarity 59.7%; Pred. No. 5.2e-16;
Matches 89; Conservative 26; Mismatches 34; Indels 0; Gaps 0;

QY 1 ATGGCCCGTGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCGCTGCTCAACGCG 60
DB 1 ATGGCNCCTGGTNCARVNTGYWSNGTNTTYYACNGTNAAYGCGNTGYTNAAYGNG 60
QY 61 TCGAGCTGCTGTGGCGCTCGCGGCTCCGCGCGCGCGCGCGCGCGCGCACCTGTGCG 120
DB 61 WSNCARVNTGCGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGACNTGYGNG 120
QY 121 TCGAGGATGAAGCGGCTGCCGACCCG 149

Query Match 59.6%; Score 88.8; DB 6; Length 2217;
Best Local Similarity 53.8%; Pred. No. 3.3e-12;
Matches 78; Conservative 25; Mismatches 42; Indels 0; Gaps 0;

QY 1 ATGGCCCGTGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCGCTGCTCAACGCG 60
DB 1 ATGGCNCCTGGTNCARVNTGYWSNGTNTTYYACNGTNAAYGCGNTGYTNAAYGNG 60
QY 61 TCGAGCTGCTGTGGCGCTCGCGGCTCCGCGCGCGCGCGCGCGCGCACCTGTGCG 120
DB 61 WSNCARVNTGCGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGACNTGYGNG 120
QY 121 TCGAGGATGAAGCGGCTGCCGAC 145
DB 121 TCGMGNGGNGTNGCNGCNGCNGCNG 145

```


RESULT 12
AA18135
ID AAS18135 standard; cDNA; 2214 BP.
XX
AC AAS18135;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DCRS8 reverse translation generic cDNA.
XX
KW Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; ss;
KW Gene therapy; protein therapy; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200190358-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016767.
XX
PR 24-MAY-2000; 2000US-0206862P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM;
XX
DR WPI; 2002-106198/14.
XX
PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
PT useful for detecting antibodies generated in response to presence of
PT increased protein levels or immunological disorders.
XX
PS Disclosure; Page 25-26; 148pp; English.
XX
CC The invention relates to primate and rodent DNAX cytokine receptor
CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
CC receptors, or their portions may be useful as phosphate labelling enzymes
CC to label general or specific substrates. The subunits may also be
CC functional immunogens to elicit recognising antibodies, or antigens
CC capable of binding antibodies. A combination, e.g., including a DCRS can
CC be used as an immunogen for the production of antisera or antibodies
CC capable of distinguishing between other cytokine receptor family members.
CC A purified DCRS can also be used as a reagent to detect antibodies
CC generated in response to the presence of elevated levels of expression,
CC or immunological disorders which lead to antibody production to the
CC endogenous receptor. This sequence represents human DCRS8 reverse
CC translation generic cDNA
SQ Sequence 2214 BP; 371 A; 223 C; 358 G; 287 T; 0 U; 975 Other;
Query Match 56.1%; Score 83.6; DB 6; Length 2214;
Best Local Similarity 51.0%; Pred. No. 6e-11; Mismatches 0; Gaps 0;
Matches 74; Conservative 24; Indels 47; Indels 0; Gaps 0;
QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGCTCAACGCTCCCTCAACGGC 60
Db 1 ATGGCCNCCNTGGYTCNCARTYNTGYWSNGINTYTYTACNGTNAAYGNTGYTNAAYGNN 60
QY 61 TCGCAGCTGGCTGTGGCGGCTCGCGCGGTCGGCGCGGCGCGCGCGCGCGCGCGCGCGC 120
Db 61 WNCARYTNGCTNGTNGCNGCNGGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNG 120
QY 121 TCGAGGATGAACGGCTGCCCGAC 145
Db 121 TGGNNNGNGTNGCNGCNGCNGCNGSNM 145
RESULT 13
AD123928
ID AD123928 standard; DNA; 18876 BP.
XX
AC AD123928;

RESULT 11
ABA95038
ID ABA95038 standard; DNA; 2217 BP.
XX
AC ABA95038;
XX
DT 20-MAY-2002 (first entry)
XX
DE Murine cytokine receptor, Zcytor18 degenerate coding sequence.
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; mouse; ds.
XX
OS Mus sp.
XX
PN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao Z;
XX
DR WPI; 2002-217048/27.
XX
PR P-PSDB; ABB07630.
XX
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX
PS Disclosure; Page 118-119; 119pp; English.
XX
CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumor growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC murine Zcytor18 degenerate coding sequence
SQ Sequence 2217 BP; 362 A; 236 C; 365 G; 289 T; 0 U; 965 Other;
Query Match 58.9%; Score 87.8; DB 6; Length 2217;
Best Local Similarity 53.1%; Pred. No. 5.8e-12;
Matches 77; Conservative 26; Mismatches 42; Indels 0; Gaps 0;
QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGCTCAACGCTCCCTCAACGGC 60
Db 1 ATGGCCNCCNTGGYTCNCARTYNTGYWSNGINTYTYTACNGTNAAYGNTGYTNAAYGNN 60
QY 61 TCGCAGCTGGCTGTGGCGGCTCGCGCGGTCGGCGCGGCGCGCGCGCGCGCGCGCGCGC 120
Db 61 WNCARYTNGCTNGTNGCNGCNGGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNGNG 120
QY 121 TCGAGGATGAACGGCTGCCCGAC 145
Db 121 TGGMGNGNGTNGCNGCNGCNGCNGSNM 145

XX 22-APR-2004 (first entry)
 DT Streptomyces refuineus 024A locus ORF4.
 DE
 XX antimicrobial; fungicide; virucide; gene therapy; lipopeptide synthesis;
 KW A54145; NRRL 3143; antimicrobial; antifungal; antiviral;
 KW biosynthetic locus; 024A; ORF4; gene; ds.
 XX Streptomyces refuineus.
 OS
 XX US2003198981-A1.
 PN 23-OCT-2003.
 PD
 XX 24-DEC-2002; 2002US-00329079.
 PF
 XX 26-DEC-2001; 2001US-0342133P.
 PR 17-APR-2002; 2002US-0372789P.
 PR 03-SEP-2002; 2002US-00232370.
 XX (ECOP-) ECOPIA BIOSCIENCES INC.
 PA Farnet CM, Staffa A, Zazopoulos E;
 XX WPI; 2003-852784/79.
 DR P-PSDB; ADI23927.
 DR
 XX New isolated, purified or enriched nucleic acid, useful for synthesizing
 PT lipopeptides, particularly from the biosynthetic locus A54145 and NRRL
 PT 3143, that exhibits antimicrobial, antifungal or antiviral activity.
 XX Example 4; SEQ ID NO 42; 69pp; English.
 PS
 XX The invention describes an isolated, purified or enriched nucleic acid
 CC (1) comprising: any of 4 fully defined sequences (SEQ. ID NO: 1, 6, 17
 CC and 34), and their coding regions; a nucleic acid having at least 75%
 CC sequence identity to a nucleic acid of (a); or complements of (a) or (b).
 CC The methods and compositions of the present invention are useful for
 CC synthesizing lipopeptides, particularly A54145 and NRRL 3143, exhibiting
 CC antimicrobial, antifungal or antiviral activity. This sequence represents
 CC ORF4 of the Streptomyces refuineus 024A (or NRRL 3143) biosynthetic
 CC locus.
 XX
 SQ Sequence 18876 BP; 2128 A; 7584 C; 7023 G; 2141 T; 0 U; 0 Other;
 Query Match 27.9%; Score 41.6; DB 10; Length 18876;
 Best Local Similarity 55.6%; Pred. No. 0.89;
 Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 2 TGGCCCGGTGCTGAGCTCTGCTCTTTTACGGTCAACGCCCTGCTCAACGGCT 61
 Db 2636 TGGCGCAGCGCTGCTGACCGTGCAGGAACGGCGCGGCGACCGCAGGCTCGTCGGCT 2695
 QY 62 CCGAGCTGGCTGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
 Db 2696 ACCTGGTCCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 121
 QY 122 GGAGGATGAAGCGGCTGCCCGAC 145
 Db 2756 GCGGAGGCTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 2779
 RESULT 14
 ID ADI23920
 XX ADI23920 standard; DNA; 61944 BP.
 XX
 AC ADI23920;
 XX
 DT 22-APR-2004 (first entry)
 DE Streptomyces refuineus 024A locus (NRRL 3143).
 XX

KW antimicrobial; fungicide; virucide; gene therapy; lipopeptide synthesis;
 KW A54145; NRRL 3143; antimicrobial; antifungal; antiviral;
 KW biosynthetic locus; 024A; ds.
 XX Streptomyces refuineus.
 OS
 XX US2003198981-A1.
 PN 23-OCT-2003.
 PD
 XX 24-DEC-2002; 2002US-00329079.
 PF
 XX 26-DEC-2001; 2001US-0342133P.
 PR 17-APR-2002; 2002US-0372789P.
 PR 03-SEP-2002; 2002US-00232370.
 XX (ECOP-) ECOPIA BIOSCIENCES INC.
 PA Farnet CM, Staffa A, Zazopoulos E;
 XX WPI; 2003-852784/79.
 DR
 XX New isolated, purified or enriched nucleic acid, useful for synthesizing
 PT lipopeptides, particularly from the biosynthetic locus A54145 and NRRL
 PT 3143, that exhibits antimicrobial, antifungal or antiviral activity.
 XX Claim 1; SEQ ID NO 34; 69pp; English.
 PS
 XX The invention describes an isolated, purified or enriched nucleic acid
 CC (1) comprising: any of 4 fully defined sequences (SEQ. ID NO: 1, 6, 17
 CC and 34), and their coding regions; a nucleic acid having at least 75%
 CC sequence identity to a nucleic acid of (a); or complements of (a) or (b).
 CC The methods and compositions of the present invention are useful for
 CC synthesizing lipopeptides, particularly A54145 and NRRL 3143, exhibiting
 CC antimicrobial, antifungal or antiviral activity. This sequence represents
 CC the Streptomyces refuineus 024A (or NRRL 3143) biosynthetic locus.
 XX
 SQ Sequence 61944 BP; 7372 A; 24375 C; 22809 G; 7388 T; 0 U; 0 Other;
 Query Match 27.9%; Score 41.6; DB 10; Length 61944;
 Best Local Similarity 55.6%; Pred. No. 0.95;
 Matches 80; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 2 TGGCCCGGTGCTGAGCTCTGCTCTTTTACGGTCAACGCCCTGCTCAACGGCT 61
 Db 7696 TGGCGCAGCGCTGCTGACCGTGCAGGAACGGCGCGGCGACCGCAGGCTCGTCGGCT 7755
 QY 62 CCGAGCTGGCTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCGGTGCGCT 121
 Db 7756 ACCTGGTCCCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 7815
 QY 122 GGAGGATGAAGCGGCTGCCCGAC 145
 Db 7816 GCGGAGGCTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 7839
 RESULT 15
 ID ACA26238/c
 XX ACA26238 standard; DNA; 567 BP.
 AC ACA26238;
 XX
 DT 19-JUN-2003 (first entry)
 DE Prokaryotic essential gene #7895.
 XX
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 XX Burkholderia mallei.
 OS
 XX WO200277183-A2.
 PN
 XX

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| Result No. | Score | Query | | | DB | ID | Description |
|------------|-------|-------|--------|------|----------------------|--------------------|-------------|
| | | Match | Length | Time | | | |
| C 1 | 38 | 25.5 | 2262 | 4 | US-09-949-016-5805 | Sequence 5805, Ap | |
| C 2 | 38 | 25.5 | 84870 | 4 | US-09-949-016-17547 | Sequence 17547, Ap | |
| C 3 | 37.8 | 25.4 | 72704 | 4 | US-09-902-540-1273 | Sequence 1273, Ap | |
| 5 | 36.6 | 24.6 | 50109 | 4 | US-09-949-016-14112 | Sequence 14112, Ap | |
| | 35.6 | 23.9 | 1674 | 4 | US-09-252-991A-1645 | Sequence 1645, Ap | |
| C 6 | 35.6 | 23.9 | 1785 | 4 | US-09-252-991A-1528 | Sequence 1528, Ap | |
| C 7 | 34.4 | 23.1 | 1437 | 4 | US-09-902-540-3148 | Sequence 3148, Ap | |
| C 8 | 34.4 | 23.1 | 19598 | 4 | US-09-902-540-1143 | Sequence 1143, Ap | |
| C 9 | 34.2 | 23.0 | 531 | 4 | US-09-252-991A-8317 | Sequence 8317, Ap | |
| C 10 | 34.2 | 23.0 | 1092 | 4 | US-09-252-991A-14341 | Sequence 14341, Ap | |
| 11 | 34.2 | 23.0 | 1167 | 4 | US-09-252-991A-14278 | Sequence 14278, A | |
| C 12 | 34.2 | 23.0 | 1332 | 1 | US-08-660-765A-3 | Sequence 3, Appli | |
| C 13 | 34.2 | 23.0 | 94156 | 4 | US-09-949-016-12388 | Sequence 12388, A | |
| C 14 | 34.2 | 23.0 | 102406 | 4 | US-09-949-016-14673 | Sequence 14673, A | |
| C 15 | 33.8 | 22.7 | 1494 | 4 | US-09-902-540-6461 | Sequence 6461, Ap | |
| C 16 | 33.8 | 22.7 | 1664 | 4 | US-09-902-540-452 | Sequence 452, App | |
| 17 | 33.8 | 22.7 | 3126 | 3 | US-09-392-184-7 | Sequence 7, Appli | |
| 18 | 33.6 | 22.6 | 1455 | 4 | US-09-489-039A-4834 | Sequence 4834, Ap | |
| 19 | 33.4 | 22.4 | 603 | 4 | US-09-252-991A-5826 | Sequence 5826, Ap | |
| 20 | 33.4 | 22.4 | 1461 | 4 | US-09-252-991A-5911 | Sequence 5911, Ap | |
| C 21 | 33.4 | 22.4 | 2796 | 4 | US-09-252-991A-5979 | Sequence 5979, Ap | |
| C 22 | 33.2 | 22.3 | 22761 | 4 | US-09-902-540-12119 | Sequence 1219, Ap | |
| C 23 | 33 | 22.1 | 2558 | 4 | US-09-902-540-6342 | Sequence 6342, Ap | |
| C 24 | 33 | 22.1 | 2560 | 4 | US-09-902-540-400 | Sequence 400, App | |
| 25 | 32.8 | 22.0 | 468 | 4 | US-09-252-991A-3702 | Sequence 3702, Ap | |
| C 26 | 32.8 | 22.0 | 513 | 4 | US-09-252-991A-3811 | Sequence 3811, Ap | |
| 27 | 32.8 | 22.0 | 744 | 4 | US-09-252-991A-3651 | Sequence 3651, Ap | |

;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 17547
;; LENGTH: 84870
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)-(84870)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17547

Query Match 25.5%; Score 38; DB 4; Length 84870;
Best Local Similarity 58.2%; Pred. No. 1.5;
Matches 85; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 3 GGCCCGGTGGTGGAGCTGCTGCTCTTTTACGGTCAACGGCTCGCTCAACGGCTC 62
DB 2212 GGACATGGTGTGCTGCTCTCTGGTGGCATCTCTCACTCCCGCGCTCAAC-GCTG 2154

QY 63 CGAGCTGGCTGGCGCTGGCGGTCCGCGCGCGGGCGCGGCGGACACTGTGGCTG 122
DB 2153 GAGCGCGGGGTGGCGGGGGGGCTTCGGGCGCGGCGGACTCCGCGCGCTGGCTTG 2094

QY 123 GAGGATGAAGCGGTGCGCCGACCC 148
DB 2093 CCGGAGACCGGCGGCTCGGCCAC 2068

RESULT 3
US-09-902-540-1273/c
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match 25.4%; Score 37.8; DB 4; Length 72704;
Best Local Similarity 55.8%; Pred. No. 1.6;
Matches 72; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 21 CTGCTCCGCTCTTTTACGGTCAACGGCTCGCTCAACGGCTCGAGCTGGCTGTGGCGCG 80
DB 24848 CAGCCCTTGTGTGACGCGCGCGCGGACAGCGCGAGCTCTCGCAGAAGGCGCGGGTGT 24789

QY 81 TGGCGGGTCCGCGCGCGCGCGGCGCGGACACTGTGCTGGAGGATCAAGCGGCTGC 140

DB 24788 CAGCGGCTCCGCTCCATCCAGCGCGCGGCTTGGCGAAGCGCGCGCGCGCGG 24729
QY 141 CCGACCCCG 149
DB 24728 CGCACACG 24720

RESULT 4
US-09-949-016-14112
; Sequence 14112, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14112
; LENGTH: 50109
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(50109)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14112

Query Match 24.6%; Score 36.6; DB 4; Length 50109;
Best Local Similarity 60.6%; Pred. No. 3.1;
Matches 60; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 12 GCTGAGCTGTGCTCCGCTCTTTTACGGTCAACGGCTCGCTCAACGGCTCGCAGCTGGC 71
DB 2069 GCTGAACCTGCGCGCGCTCTTCGATGTCACAAAGACCGCTTCAACCACTTCAGTGGCG 2128

QY 72 TGTGCGCGCTGCGGGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 110
DB 2129 CGCGGCGGAGCGGGGCTGCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2167

RESULT 5
US-09-252-991A-1645
; Sequence 1645, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1645
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1645

Query Match 23.9%; Score 35.6; DB 4; Length 1674;

; PRIOR APPLICATION NUMBER: US 60/094,190
 ;
 ; PRIOR FILING DATE: 1998-07-27
 ;
 ; NUMBER OF SEQ ID NOS: 33142
 ;
 ; SEQ ID NO 8317

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; LENGTH: 531
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8317

Query Match      23.0%; Score 34.2; DB 4; Length 531;
Best Local Similarity 55.5%; Pred. No. 8.9;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 15 GCAGCTCTGCTCGCTCTCTTTACGGTCAACCGCTGCTCAACGGCTGCGAGCTGGCTGT 74
   |||||
Db 220 GCTGACCGCCCTGTGTTTCGGAACGCGCATGGCTTGCTCGGCTGCTCCACCTGGGCT 161
   |||||

QY 75 GCGCCCTGCGGGTCCGGCGCGCGCGGGCGCCGACACCTGTGCTGGAGATCAAG 133
   |||||
Db 160 GCGTCTGCGCCAGGCTGTGTCGGCGAGCGGCGCGGGTATCAGCGGGTTCGGCCTGGACG 102

RESULT 10
US-09-252-991A-14341/c
; Sequence 14341, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14341
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14341

Query Match      23.0%; Score 34.2; DB 4; Length 1092;
Best Local Similarity 55.5%; Pred. No. 9.3;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 6 CCGGTGGCTGAGCTCTGCTCGCTCTTTTACGGTCAACGGCTGCTCAACGGCTCGCA 65
   |||||
Db 907 CTGTGTGAGCTCCAGGTCACCGCGCTGTCGATGCTCTTCGGCATCTCTCATCGCCCTGT 848
   |||||

QY 66 GCTGGCTGTGGCGCTGCGGGTCCGGCGCGCGGGCGCGGACACCTGTGGCTGGA 124
   |||||
Db 847 CCTGGCTTTCGCCGCTGCGCGGTAAACCGCCGCTGCGCGCGCGCGGAGGCTGGA 789
   |||||

RESULT 11
US-09-252-991A-14278
; Sequence 14278, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14278
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
```

```
US-09-252-991A-14278

Query Match      23.0%; Score 34.2; DB 4; Length 1167;
Best Local Similarity 55.5%; Pred. No. 9.4;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 6 CCGGTGGCTGAGCTCTGCTCGCTCTTTTACGGTCAACGGCTGCTCAACGGCTCGCA 65
   |||||
Db 567 CTGTGTGAGCTCCAGGTCACCGCGCTGTCGATGCTCTTCGGCATCTCTCATCGCCCTGCT 626
   |||||

QY 66 GCTGGCTGTGGCGCTGCGGGTCCGGCGCGGGCGCGGACACCTGTGGCTGGA 124
   |||||
Db 627 CTTGGCTTTCGCCGCTGCGGGTAAACCGCGCTGCGCGCGCGCGGAGCCTGGA 685
   |||||

RESULT 12
US-08-660-765A-3/c
; Sequence 3, Application US/08660765A
; Patent No. 5652125
; GENERAL INFORMATION:
; APPLICANT: SCOTTI, Claudio
; APPLICANT: HUTCHINSON, Charles R.
; APPLICANT: COLOMBO, Anna L.
; APPLICANT: FILIPPINI, Silvia
; TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIKAIIDO, MARWELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 - G
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,765A
; FILING DATE: 10-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BERMAN, Richard J.
; REGISTRATION NUMBER: 39,107
; REFERENCE/DOCKET NUMBER: P1615-6005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1332 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-660-765A-3

Query Match      23.0%; Score 34.2; DB 1; Length 1332;
Best Local Similarity 56.8%; Pred. No. 9.5;
Matches 63; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 ATGGCCCCGTGGTGGAGCTCTGCTCGCTCTTTTACGGTCAACGGCTGCTCAACGGC 60
   |||||
Db 602 ATGTCCCGCGGCTGCGCCCGCACCGCTCCAGCGTCCAGGTGAGCACTCGGCCAGCGG 543
   |||||

QY 61 TCGCAGCTGGCTGTGGCGGCTGGGGGTCCGGCGCGCGGGCGCGGCGCGAC 111
   |||||
Db 542 TCGTCGCGCAGCTCGGGCGGTTTCGGGTGAGAGGCGCGCGGACCGCGTC 492
   |||||

RESULT 13
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```
US-09-949-016-12388/c
; Sequence 12388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12388
; LENGTH: 94156
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(94156)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12388

Query Match      23.0%; Score 34.2; DB 4; Length 94156;
Best Local Similarity 56.8%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 39 GGTCAACGCTCCTCAACGGCTCGAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGC 98
DB 30991 GGTCAACGCTCCTCAACGGCTCGAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGC 98

QY 39 GGTCAACGCTCCTCAACGGCTCGAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGC 98
DB 30991 GGTCAACGCTCCTCAACGGCTCGAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGC 98

QY 99 GCGGGGCGCGCACACCTGTGGCTGGAGGATGAAGCGGTGCCCGACCCCG 149
DB 30931 CCGGCCAGCGCCCGCTCGGGAGGAGGTGGGGGGGTGAGCCCGCCCG 30881

RESULT 14
US-09-949-016-14673/c
; Sequence 14673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14673
; LENGTH: 102406
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(102406)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14673

Query Match      23.0%; Score 34.2; DB 4; Length 102406;
Best Local Similarity 56.8%; Pred. No. 13;
Matches 63; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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QY 39 GGTCAACGCTCCTCAACGGCTCGAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGC 98
DB 30991 GGTCAACGCTCCTCAACGGCTCGAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGC 98

QY 99 GCGGGGCGCGCACACCTGTGGCTGGAGGATGAAGCGGTGCCCGACCCCG 149
DB 30931 CCGGCCAGCGCCCGCTCGGGAGGAGGTGGGGGGGTGAGCCCGCCCG 30881

RESULT 15
US-09-902-540-6461
; Sequence 6461, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6461
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(1494)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-6461

Query Match      22.7%; Score 33.8; DB 4; Length 1494;
Best Local Similarity 58.4%; Pred. No. 12;
Matches 59; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 2 TCGCCCGGTGGCTGCGAGCTGCTCGTCTTTTACGGTCAACGCTCGCTCAACGGCT 61
DB 512 TGGACCGGTGCTGGCGCGCTTCGGCGACTGCAAGGACCAAGGCGGCTCATCCACT 571

QY 62 CGCAGCTGGCTGTGGCCGCTGCGCGGTCCGGCCGCGCGCG 102
DB 572 CCATGCTCCAGTGGCGGTGGAGAGCGCGTGTGTG 612

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-717-282-1_COPY_86_234

Perfect score: 149

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 126.8 | 85.1 | 585 | 4 | BG149830 nae01a12. |
| 2 | 125 | 83.9 | 230 | 2 | BP515598 UT-H-BW1- |
| 3 | 112.6 | 75.6 | 474 | 6 | CAB79041 K0971D08- |
| 4 | 112.6 | 75.6 | 665 | 2 | BB641245 BB641245 |
| 5 | 111.6 | 74.9 | 239 | 8 | CC178870 XST163 Ba |
| 6 | 110 | 73.8 | 547 | 2 | BE750478 201867 MA |
| 7 | 101.8 | 68.3 | 483 | 5 | BY152713 BY152713 |
| 8 | 99.8 | 67.0 | 724 | 5 | BP154750 BP154750 |
| 9 | 51.6 | 34.6 | 134 | 9 | CL212737 G049F09 G |
| 10 | 43.6 | 29.3 | 271 | 1 | AL450535 AL450535 |
| 11 | 43 | 28.9 | 573 | 4 | BM371103 EBR04 SQ |
| 12 | 43 | 28.9 | 854 | 2 | BF630932 HVSMB001 |
| 13 | 41.8 | 28.1 | 513 | 7 | CF260435 NCST3d04 |
| 14 | 41.8 | 28.1 | 565 | 7 | CF943197 NCST3qab9 |
| 15 | 41.8 | 28.1 | 598 | 7 | CF261081 NCST3c80 |
| 16 | 40 | 26.8 | 533 | 6 | CA259967 SCPRRT302 |
| 17 | 38.8 | 26.0 | 313 | 5 | BQ753596 Eban01 SQ |
| 18 | 38.8 | 26.0 | 454 | 5 | BQ764296 Eban01 SQ |
| 19 | 38.6 | 25.9 | 622 | 7 | CN412349 170005322 |
| 20 | 38.4 | 25.8 | 676 | 6 | CD058409 H004022S |
| 21 | 38.4 | 25.8 | 366 | 7 | CN412348 170006000 |
| 22 | 38 | 25.5 | 555 | 7 | CN412341 170005326 |
| 23 | 38 | 25.5 | 559 | 4 | BG720080 602691584 |
| 24 | 38 | 25.5 | 599 | 4 | BG720080 602691584 |

| | | | | | | |
|------|------|------|------|---|----------|---------------------|
| C 25 | 38 | 25.5 | 656 | 7 | CN412342 | CN412342 170004706 |
| C 26 | 38 | 25.5 | 666 | 7 | CN412351 | CN412351 170006000 |
| C 27 | 38 | 25.5 | 710 | 7 | CN412352 | CN412352 170006001 |
| C 28 | 38 | 25.5 | 800 | 4 | BG718697 | BG718697 602696826 |
| C 29 | 38 | 25.5 | 916 | 5 | BU509388 | BU509388 AGENCOURT |
| C 30 | 38 | 25.5 | 1001 | 2 | BE783051 | BE783051 601470628 |
| C 31 | 38 | 25.5 | 2088 | 9 | CL507788 | CL507788 SAIL_788 |
| C 32 | 37.8 | 25.4 | 398 | 8 | AZ047386 | AZ047386 nbeb0093F |
| C 33 | 37.8 | 25.4 | 526 | 4 | BI562240 | BI562240 603254956 |
| C 34 | 37.8 | 25.4 | 529 | 1 | AL829621 | AL829621 AL829621 |
| C 35 | 37.8 | 25.4 | 811 | 9 | CC660832 | CC660832 CGWDR222TH |
| C 36 | 37.6 | 25.2 | 332 | 1 | AJ679503 | AJ679503 AJ679503 |
| C 37 | 37.6 | 25.2 | 626 | 6 | CA149067 | CA149067 SCJLRZ102 |
| C 38 | 37.4 | 25.1 | 542 | 9 | CL793216 | CL793216 OR_CBA000 |
| C 39 | 37.4 | 25.1 | 603 | 9 | CL774375 | CL774375 OR_BBa008 |
| C 40 | 37.4 | 25.1 | 775 | 4 | BG610752 | BG610752 602612565 |
| C 41 | 37.4 | 25.1 | 1036 | 7 | CK213161 | CK213161 FGAS02506 |
| C 42 | 37.2 | 25.0 | 277 | 1 | AUL77782 | AUL77782 AUL77782 |
| C 43 | 37.2 | 25.0 | 319 | 1 | AV939902 | AV939902 AV939902 |
| C 44 | 37.2 | 25.0 | 478 | 5 | BU970198 | BU970198 HB13018r |
| C 45 | 37.2 | 25.0 | 487 | 5 | BU970159 | BU970159 HB13M18r |

ALIGNMENTS

RESULT 1
BG149830
LOCUS nae01a12.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3434014 3',
DEFINITION mRNA sequence.
ACCESSION BG149830
VERSION BG149830.1 GI:12661860
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 585)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 492.
Location/Qualifiers
1. 585
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3434014"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/note="Organ: ovary; Vector: pRTT3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TCGTACCAATCTGAAGTGGAGCGCGCGGACATTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pRTT3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

/lab host="DH10B"
 /clone lib="NIA Mouse Neural Stem Cell (Undifferentiated)
 cDNA Library (Long)"
 /notes="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
 NotI; Mouse cDNA project by the Laboratory of Genetics,
 National Institute on Aging (NIA), Intramural Research
 Program, NIH (http://igsn.grc.nia.nih.gov/cDNA). This is
 a long-transcript enriched cDNA library (Ref. Genome Res.
 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
 obtained from Dr. Angelo L. Vescovi (Institute for Stem
 Cell Research, Italy). Double-stranded cDNAs were
 synthesized with an oligo(dT) primer [Invitrogen:
 5'-pGATGTTCTAGATCGGCGCGCGCTTTTCTTTT-3'] from
 2.0 Microgram of total RNA, treated with T4 DNA
 polymerase, and purified by ethanol-precipitation. The
 cDNAs were ligated to lone-linker L1-Sal4, purified by
 phenol/chloroform, and separated from free linkers by
 Centricon 100. Then, the cDNAs were amplified by
 long-range high fidelity PCR using Ex Taq polymerase
 (Takara) with a primer Sal4-S. The products were purified
 by phenol/chloroform and Centricon 100. The cDNAs were
 digested with SalI and NotI enzymes and cloned into
 SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.
 coli host was transformed with the ligation mixture by the
 standard chemical method. The average insert size is about
 3.8 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 75.6%; Score 112.6; DB 6; Length 474;
 Best Local Similarity 86.7%; Pred. No. 9.1e-18;
 Matches 124; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 ATGGCCCGGTGGCTGAGTCTGCTCGCTCTTTTACGGTCAACCGCTGCTCAACGGC 60
 DB 26 ATGGCCCGGTGGCTGAGTCTGCTCTTTTACGGTCAACCGCTGCTCAACGGC 85
 QY 61 TCGCAGTGGCTGTCGCGTGGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 86 TCGCAGTGGCTGTCGCGTGGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 145
 QY 121 TGGAGGATGAACCGCTGCTCCG 143
 DB 146 TGGAGGAGTGGCGCGCGCGCGAG 168

RESULT 4

BB641245
 LOCUS BB641245 RIKEN full-length enriched, 10 days neonate cortex Mus
 DEFINITION musculus cDNA clone A830013G13 5', mRNA sequence.
 ACCESSION BB641245
 VERSION BB641245.1 GI:16476370
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Hara A., Hiramoto K., Carninci P., Fukuda S., Furuno M., Hanagaki T.,
 Kono H., Kouda M., Koya S., Matsuyama T., Miyazaki A., Nomura K.,
 Ohno M., Okazaki Y., Okido T., Saito R., Sakai C., Sakai K.,
 Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T.,
 Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F.,
 Takeda Y., Tanaka T., Toya T., Muramatsu M. and Hayashizaki Y.
 RIKEN Mouse ESTs (Arakawa T., et al. 2001)
 Unpublished (2001)

TITLE

JOURNAL Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222

Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
 Itoh M., Konno H., Okazaki Y., Muramatsu M. and Hayashizaki Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T.,
 Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A.
 and Hayashizaki Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno H., Fukunishi Y., Shibata K., Itoh M., Carninci P.,
 Sugahara Y. and Hayashizaki Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo S., Shinagawa A., Saito T., Kiyosawa H., Yamanaka T.,
 Aizawa K., Fukuda S., Hara A., Itoh M., Kawai J., Shibata K. and
 Hayashizaki Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.

FEATURES

source

1..665
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="A830013G13"
 /tissue_type="cortex"
 /dev_stage="10 days neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 10 days neonate
 cortex"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 20.0 and subtraction to Rot = 459.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCC
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a
 modified pBluescript KS(+) after bulk excision from lambda
 FLC I."

ORIGIN

Query Match 75.6%; Score 112.6; DB 2; Length 665;
 Best Local Similarity 86.7%; Pred. No. 9.1e-18;
 Matches 124; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 ATGGCCCGGTGGCTGAGTCTGCTCGCTCTTTTACGGTCAACCGCTGCTCAACGGC 60
 DB 33 ATGGCCCGGTGGCTGAGTCTGCTCTTTTACGGTCAACCGCTGCTCAACGGC 92
 QY 61 TCGCAGTGGCTGTCGCGTGGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 93 TCGCAGTGGCTGTCGCGTGGCGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 152
 QY 121 TGGAGGATGAACCGCTGCTCCG 143
 DB 153 TGGAGGAGTGGCGCGCGCGAG 175

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RESULT 5
CC178870          239 bp      mRNA      linear      GSS 02-MAY-2003
LOCUS             XST163 BayGenomics Gene Trap Library pGTLTpfs Mus musculus cDNA,
DEFINITION        mRNA sequence.
ACCESSION         CC178870
VERSION           CC178870.1  GI:30317421
KEYWORDS          Mus musculus (house mouse)
SOURCE            GSS.
ORGANISM          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 239)
BayGenomics.
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINE&KEY=XST163
Class: Gene Trap.
Location/Qualifiers
1..239
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/strain="129 ola"
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/sex="Male"
/cell_type="Embryonic stem cell"
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/note="Vector: pGTLTpfs"

FEATURES
source
Location/Qualifiers
1..239
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ORIGIN
Query Match      74.9%; Score 111.6; DB 8; Length 239;
Best Local Similarity 92.9%; Pred. No. 1.6e-17;
Matches 117; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 ATGGCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 60
|||||
Db 114 ATGGCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACCTGTCAACGCTGTCTCAACGGC 173
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QY 61 TCGCAGCTGGCTGGCTGGCGGCTCCGGCCGCGCGCGCGCGCGACACCTGTGGC 120
|||||
Db 174 TCGCAGCTGGCAGTGGCCGCGGCGGCTCCGGCCGCGCGCGCGCGACACCTGTGGC 233
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QY 121 TGGAGG 126
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Db 234 TGGAGG 239

RESULT 6
BE750478          547 bp      mRNA      linear      EST 25-APR-2001
LOCUS             201867 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION
ACCESSION         BE750478
VERSION           BE750478.1  GI:10164470
KEYWORDS          Bos taurus (cow)
SOURCE            EST.
ORGANISM          Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 547)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Cassas, E., Wray, J.E., White, J., Cho, J., Fahrnenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,


```

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TITLE
JOURNAL           Quackenbush, J. and Keele, J.W.
MEDLINE           Sequence evaluation of four pooled-tissue normalized bovine cDNA
PUBMED            libraries and construction of a gene index for cattle
COMMENT           Genome Res. 11 (4), 626-630 (2001)
                  21180013
                  11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAAGCAGG
Plate: 112 row: C column: 10
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."

FEATURES
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Location/Qualifiers
1..547
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/lab_host="DH10B"
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Library made from pooled tissue from day 20 and day 40
embryos."

ORIGIN
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Best Local Similarity 92.1%; Pred. No. 4e-17;
Matches 116; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGC 60
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Db 17 ATGGCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCTGCTCAACGGT 76
|||||

QY 61 TCGCAGCTGGCTGTGGCGGCTGGCGGGTCCGGCCGCGCGCGCGACACCTGTGGC 120
|||||
Db 77 TCGCAGCTGGCGGCTGGCTGCAGGGGCTCCAGAGAGCGGGCGCGACACCTGTGGC 136
|||||

QY 121 TGGAGG 126
|||||
Db 137 TGGAGG 142

RESULT 7
BY152713          483 bp      mRNA      linear      EST 31-DEC-2002
LOCUS             BY152713 RIKEN full-length enriched, B16 F10Y cells Mus musculus
DEFINITION        cDNA clone G370032A13 5', mRNA sequence.
ACCESSION         BY152713
VERSION           BY152713.1  GI:26289242
KEYWORDS          EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 483)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chotha, C., Corbani, I.E., Cousins, S., Della, E., Dragani, T.A.,
Flathner, C., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,


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Db      158 TGGAGGGAGTGGGGCCGCCG 180
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CL212737 134 bp mRNA linear GSS 30-JUN-2004
G049F09 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
CL212737 mRNA sequence.
ACCESSION CL212737
VERSION CL212737.1 GI:40729638
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 134)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,P.,
Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
JOURNAL 22810117
MEDLINE 12904583
PUBMED
COMMENT Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
U3CEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G049F09' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 16755
Class: Gene Trap.
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Location/Qualifiers
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/clone="G049F09"
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/cell_type="Embryonic stem cell"
/cell_line="ES cells [C57BL/6J x 129Sv] F1"
/clone_lib="GGTC Gene Trap Library GV07C05"
/note="Vector: U3CEO"

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Query Match 34.6%; Score 51.6; DB 9; Length 134;
Best Local Similarity 70.3%; Pred. No. 0.012;
Matches 83; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCGCTCCTCAACGCG 60
Db 15 ATGGAACAGTGGATGCGATTTTCATATTCCTCAATG-AAAACCCCTCTCGTAGT 73
QY 61 TCGCAGCTGGCTGTGCGCGCTGGCGGGTCCGCGCGCGCGCGCGCGACACCTGTG 118
Db 74 TGGCAGCTGACAGTGGCCGCGACGGCTCCGCGCGCGCGCGCGACACCTGGG 131

RESULT 10
AL450535 271 bp mRNA linear EST 07-DEC-2000
LOCUS AL450535 Hordeum vulgare Barke etiolated leaves Hordeum vulgare
DEFINITION subsp. vulgare cDNA clone HK03A19u 5', mRNA sequence.
ACCESSION AL450535
VERSION AL450535.1 GI:11601943
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Db      158 TGGAGGGAGTGGGGCCGCCG 180
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CL212737 134 bp mRNA linear GSS 30-JUN-2004
G049F09 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
CL212737 mRNA sequence.
ACCESSION CL212737
VERSION CL212737.1 GI:40729638
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 134)
Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,P.,
Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
A large-scale, gene-driven mutagenesis approach for the functional
analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
JOURNAL 22810117
MEDLINE 12904583
PUBMED
COMMENT Contact: GGTC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
U3CEO gene trap. Sequence tag generated by 5'RACE. Additional
sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
clone_id=G049F09' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
1' Inhouse Sequence Identifier: 16755
Class: Gene Trap.
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1..134
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Query Match 34.6%; Score 51.6; DB 9; Length 134;
Best Local Similarity 70.3%; Pred. No. 0.012;
Matches 83; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATGGCCCCGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCGCTCCTCAACGCG 60
Db 15 ATGGAACAGTGGATGCGATTTTCATATTCCTCAATG-AAAACCCCTCTCGTAGT 73
QY 61 TCGCAGCTGGCTGTGCGCGCTGGCGGGTCCGCGCGCGCGCGCGACACCTGTG 118
Db 74 TGGCAGCTGACAGTGGCCGCGACGGCTCCGCGCGCGCGCGCGACACCTGGG 131

RESULT 10
AL450535 271 bp mRNA linear EST 07-DEC-2000
LOCUS AL450535 Hordeum vulgare Barke etiolated leaves Hordeum vulgare
DEFINITION subsp. vulgare cDNA clone HK03A19u 5', mRNA sequence.
ACCESSION AL450535
VERSION AL450535.1 GI:11601943
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 271)
Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: M13uni primer for 5'end.
FEATURES
Location/Qualifiers
1..271
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/sub_species="vulgare"
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/clone="HK03A19u"
/tissue_type="etiolated leaves"
/lab_host="XL1Blue"
/clone_lib="Hordeum vulgare Barke etiolated leaves"
/note="Vector: pBluescript SK-; Site.1: SalI; Site.2:
NotI; mRNA was made from etiolated leaves of spring barley
variety 'Barke', a high quality malting variety. Plants
were grown on filterpaper for 6 d at 25 C in the dark.
Leaves were harvested at daylight conditions. Sal-Adaptor
Sequence: TCGACCCAGGCGTCG Average insert size is 1 kb
Sequence trimming: Vector sequences and sequence ends were
trimmed from the 5'-and 3'-end until a 50 bp window
contains less than two ambiguities. The maximum length was
set to 700 bp."

ORIGIN
Query Match 29.3%; Score 43.6; DB 1; Length 271;
Best Local Similarity 60.9%; Pred. No. 1.1;
Matches 70; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 GCCCGGTGGCTGCAGCTCTGCTCCGCTCTTTTACGGTCAACGCGCTCCTCAACGCGCTCG 63
Db 65 GGGCGCGGCTGCGCGCGCGCCCTCGCCGTCGCCGCCACCGCGCGGTCTCCGGCCCC 124
QY 64 CAGCTGGCTGTGGCGCGCTGCGCGCGGTCCGCGCGCGCGCGCGCGACACCTGTG 118
Db 125 GAGCAAGATGTCGCTCGGTGAAGCGCGCGCGCGAGCTGGCGCGCGCTG 179

RESULT 11
BM371103 573 bp mRNA linear EST 23-JUL-2002
LOCUS BM371103 Hordeum vulgare subsp. vulgare cDNA clone EBr004_SQ003_H20 5', mRNA
DEFINITION subsp. vulgare subsp. vulgare cDNA clone EBr004_SQ003_H20 5', mRNA
sequence.
ACCESSION BM371103
VERSION BM371103.2 GI:21949377
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 573)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Jan 10, 2002 this sequence version replaced gi:18114493.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426

```


4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Contact David Sibley (toxost@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.
 Seq primer: T3
 High quality sequence stop: 509.
 Location/Qualifiers

FEATURES

source

1. .513

/organism="Neospora caninum"

/mol_type="mRNA"

/db_xref="taxon:29176"

/dev_stage="Tachyzoite"

/lab_host="Electron Blue cells (Stratagene)"

/clone_lib="Nc-LIV Tachyzoite cDNA Library"

/note="Vector: pBluescript II SK+Vector type: plasmid;

Site 1: EcoRI; Site 2: XhoI; The cDNA library was

constructed by Keliang Tang, and Robert Cole at Washington

University. cDNA was synthesized from Poly(A)⁺ mRNA using

an oligo-d(T) primer containing a XhoI site. Following

second strand synthesis, EcoRI adapters were ligated to

the cDNA, and products were size-selected on sephacryl

S500. The cDNA were directionally cloned into the

EcoRI/XhoI prepared pBluescript II SK+ vector, and

electroporated into Electron Blue cells (Stratagene).

The library may contain a small percentage of host or

bacterial contaminants."

ORIGIN

Query Match 28.1%; Score 41.8; DB 7; Length 513;

Best Local Similarity 65.6%; Pred. No. 2.9;

Matches 61; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 25 TCCGCTCTCTTTACGGTCAACGCCCTCGCTCAACGGCTCGCAGCTGGCTGTGGCCGCTGGC 84
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 Db 425 TCCGACTTCTGTGTCAGAAATCTGCTCAGTTGCTGAGAGCGCTTCGGCGCGCTGGC 366
 |||||

QY 85 GGGTCGGCGCGCGCGGGGCGCCGACACCTGT 117
 |||||Db 365 GAGGCAGGCTCGCGCTTGGCGCGCCGCACTCT 333
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RESULT 14

CF943197/c

LOCUS

DEFINITION

CF943197 NCESTqab95g02.y1 Nc-1 Tachyzoite cDNA Library 2 Neospora caninum

CF943197 cDNA 5', mRNA sequence.

CF943197.1 GI:38443767

EST.

SOURCE

Neospora caninum

Neospora caninum

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Neospora.

1 (bases 1 to 565)

REFERENCE

AUTHORS

Cole, R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S.,
 Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B.,
 Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I.,
 Tsagarisvilli, R., Fedele, M., Belaygorod, L., Franklin, C.,
 Carr, L.M., Grow, A., Maguire, L., Wadkins, J., Richey, J., Waterston, R.
 and Wilson, R.

USDA-WashU Neospora EST Project

Unpublished (2000)

Contact: Sandy Clifton, Ph.D. - Neospora

USDA-WashU Neospora EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Contact David Sibley (toxost@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.

FEATURES

source

Seq primer: -40RP from Gibco.

Location/Qualifiers

1. .565

/organism="Neospora caninum"

/mol_type="mRNA"

/db_xref="taxon:29176"

/dev_stage="Tachyzoite"

/lab_host="GC10 Competent Cells (PGC)"

/clone_lib="Nc-1 Tachyzoite cDNA Library 2"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

XhoI; The cDNA library was constructed by Keliang Tang,

and Robert Cole at Washington University. cDNA was

synthesized from poly mRNA using an oligo-dT primer

containing a XhoI site. Following second strand synthesis,

EcoRI adapters were ligated to the cDNA, and products were

size-selected on sephacryl S500. The cDNA were

directionally cloned into the EcoRI/XhoI prepared

pBluescript II SK+ vector, and electroporated into GC10

Competent Cells (PGC). The library may contain a small

percentage of host or bacterial contaminants."

ORIGIN

Query Match 28.1%; Score 41.8; DB 7; Length 565;

Best Local Similarity 65.6%; Pred. No. 2.9;

Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 25 TCCGCTCTCTTTACGGTCAACGCCCTCGCTCAACGGCTCGCAGCTGGCTGTGGCCGCTGGC 84
 |||||
 Db 504 TCCGACTTCTGTGTCAGAAATCTGCTCAGTTGCTGAGAGCGCTTCGGCGCGCTGGC 445
 |||||

QY 85 GGGTCGGCGCGCGCGGGGCGCCGACACCTGT 117
 |||||Db 444 GAGGCAGGCTCGCGCTTGGCGCGCCGCACTCT 412
 |||||

RESULT 15

CF261081/c

LOCUS

DEFINITION

CF261081 NCEST3c80all.y3 Nc-LIV Tachyzoite cDNA Library Neospora caninum

CF261081 cDNA 5', mRNA sequence.

CF261081.1 GI:33588654

EST.

SOURCE

Neospora caninum

Neospora caninum

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Sarcocystidae; Neospora.

1 (bases 1 to 598)

REFERENCE

AUTHORS

Cole, R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S.,
 Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Theising, B.,
 Bowers, Y., Gibbons, M., Ritter, E., Bennet, J., Ronko, I.,
 Tsagarisvilli, R., Fedele, M., Belaygorod, L., Franklin, C.,
 Carr, L.M., Grow, A., Maguire, L., Wadkins, J., Richey, J., Waterston, R.
 and Wilson, R.

USDA-WashU Neospora EST Project

Unpublished (2000)

Contact: Sandy Clifton, Ph.D. - Neospora

USDA-WashU Neospora EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Contact David Sibley (toxost@borcim.wustl.edu) for further
 information relating to organism, libraries, or clone availability.

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1. .598

/organism="Neospora caninum"

/mol_type="mRNA"

/db_xref="taxon:29176"

/dev_stage="Tachyzoite"

/lab_host="ElectroTen Blue cells (Stratagene)"

/clone lib="NC-LIV Tachyzoite cDNA Library"
/note="Vector: pBluescript II SK+Vector type: plasmid;
Site 1: EcoRI; Site 2: XhoI; The cDNA library was
constructed by Keliang Tang, and Robert Cole at Washington
University. cDNA was synthesized from Poly(A)+ mRNA using
an oligo-d(T) primer containing a XhoI site. Following
second strand synthesis, EcoRI adapters were ligated to
the cDNA, and products were size-selected on sephacryl
S500. The cDNA were directionally cloned into the
EcoRI/XhoI prepared pBluescript II SK+ vector, and
electroporated into Electrogen Blue cells (Stratagene).
The library may contain a small percentage of host or
bacterial contaminants."

ORIGIN

| | | | | |
|-----------------------|--------|---|-------|----------------------------------|
| Query Match | 28.1%; | Score 41.8; | DB 7; | Length 598; |
| Best Local Similarity | 65.6%; | Pred. No. 2.9; | | |
| Matches | 61; | Conservative | 0; | Mismatches 32; Indels 0; Gaps 0; |
| Qy | 25 | TCGGTCTTCTTACGGTCAACGCTGCCTCAACGGCTCGAGCTGGCTGGCGCTGGC | 84 | |
| Db | 594 | TCGACTTCTCTGTGAGAAAGTCTGCCTCAGTTGCTCGAGAGCGCTTCGGCGGCTGGC | 535 | |
| Qy | 85 | GGGTCCGGCCGGCGCGGGCGCGCACCTGT | 117 | |
| Db | 534 | GAGGCAGGCTCGGCGTTGGCGCGCGCGACTCT | 502 | |

Search completed: August 16, 2005, 05:21:56
Job time : 3183 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:33:31 ; Search time 121.831 Seconds
(without alignments)
2390.439 Million cell updates/sec

Title: US-10-717-282-2
Perfect score: 4013
Sequence: 1 MAPWLQCSVFVFTVACLING.....CKADLGCRSYTDELHVAAPL 753

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 4013 | 100.0 | 753 | 5 | ABB07626 Human cyt |
| 2 | 4003 | 99.8 | 753 | 5 | ABB07627 Human cyt |
| 3 | 3325 | 97.8 | 739 | 5 | ABB07628 Human cyt |
| 4 | 3301 | 97.2 | 738 | 4 | Aau09904 Human Int |
| 5 | 3897 | 97.1 | 738 | 4 | Aau09953 Human Int |
| 6 | 3896 | 97.1 | 738 | 4 | Aau09954 Human Int |
| 7 | 3894 | 97.0 | 738 | 4 | Aau09951 Human Int |
| 8 | 3894 | 97.0 | 738 | 4 | Aau09952 Human Int |
| 9 | 3894 | 97.0 | 738 | 4 | Aau09956 Human Int |
| 10 | 3890 | 96.9 | 738 | 4 | Aau09957 Human Int |
| 11 | 3890 | 96.9 | 738 | 4 | Aau09955 Human Int |
| 12 | 3830.5 | 95.5 | 738 | 5 | Aau11355 Human DNA |
| 13 | 3708 | 92.4 | 728 | 7 | ADb65245 Human pro |
| 14 | 3703 | 92.3 | 728 | 4 | Aau04958 Human Int |
| 15 | 3703 | 92.3 | 728 | 6 | ABu72600 Human Int |
| 16 | 3703 | 92.3 | 728 | 6 | ADA43241 Human Int |
| 17 | 3703 | 92.3 | 728 | 6 | ADA43241 Human Int |
| 18 | 3703 | 92.3 | 728 | 7 | ADA49782 Human PRO |
| 19 | 3703 | 92.3 | 728 | 7 | ADA26975 Human PRO |
| 20 | 3703 | 92.3 | 728 | 7 | ADb66909 Human PRO |
| 21 | 3703 | 92.3 | 728 | 7 | ABw02061 Human IL- |
| 22 | 3703 | 92.3 | 728 | 7 | ADg97393 Human PRO |
| 23 | 3703 | 92.3 | 728 | 7 | ADl16689 Human PRO |
| 24 | 3703 | 92.3 | 728 | 8 | ADl16650 Human PRO |
| 25 | 3703 | 92.3 | 728 | 8 | ADl71310 Human IL- |

ALIGNMENTS

RESULT 1

ABB07626
ID ABB07626 standard; protein; 753 AA.

AC ABB07626;

XX 20-MAY-2002 (first entry)

XX Human cytokine receptor, Zcytor18 amino acid sequence.

XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy.

XX Homo sapiens.

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Preenell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for
inhibiting cell proliferation associated with psoriasis or tumor growth,
and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 1; Page 2; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide
designated Zcytor18. The Zcytor18 polypeptides can be expressed by
standard recombinant methodology. The polypeptides can be used to inhibit
cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
therapy techniques. Zcytor18 oligonucleotide probes are useful for in
vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial

| | | | | | | |
|----|--------|------|-----|---|-----------|---------------------|
| 26 | 3703 | 92.3 | 739 | 4 | AAU10602 | AAU10602 Human int |
| 27 | 3387 | 84.4 | 739 | 5 | ABB07630 | ABB07630 Murine cy |
| 28 | 3176 | 79.1 | 595 | 6 | AAE33485 | AAE33485 Human REM |
| 29 | 3170 | 79.0 | 595 | 4 | ABU53091 | ABU53091 Human tra |
| 30 | 3166 | 78.9 | 595 | 5 | ABP69026 | ABP69026 Human pol |
| 31 | 2699.5 | 67.3 | 554 | 5 | AAU91330 | AAU91330 Human nov |
| 32 | 1337 | 33.3 | 296 | 4 | AAU10601 | AAU10601 5' portio |
| 33 | 312 | 7.8 | 866 | 2 | AAW04185 | AAW04185 Human int |
| 34 | 312 | 7.8 | 866 | 2 | AAW61272 | AAW61272 Human int |
| 35 | 312 | 7.8 | 866 | 2 | AAW92409 | AAW92409 Human IL- |
| 36 | 312 | 7.8 | 866 | 3 | AAU97131 | AAU97131 Human int |
| 37 | 312 | 7.8 | 866 | 3 | AAU97181 | AAU97181 Human int |
| 38 | 312 | 7.8 | 866 | 3 | AAU03807 | AAU03807 Human int |
| 39 | 312 | 7.8 | 866 | 3 | AAU99941 | AAU99941 Human IL- |
| 40 | 312 | 7.8 | 866 | 4 | AAAB62066 | AAAB62066 Human IL- |
| 41 | 312 | 7.8 | 866 | 4 | AAU72754 | AAU72754 Human int |
| 42 | 312 | 7.8 | 866 | 5 | ABB78079 | ABB78079 Amino aci |
| 43 | 312 | 7.8 | 866 | 7 | ADD25546 | ADD25546 Binding d |
| 44 | 312 | 7.8 | 866 | 8 | ADJ88265 | ADJ88265 Human IL- |
| 45 | 312 | 7.8 | 866 | 8 | ADL24269 | ADL24269 Human IL- |

CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 amino acid sequence
XX
SQ Sequence 753 AA;
Query Match 100.0%; Score 4013; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAPWLQCSVFTYNACLSQSLAAAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFTYNACLSQSLAAAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60
Qy 61 ASRNSGLYNTFFKYDNCCTYLNPNVKGKVIADAQNITISQYACHQVAVTILWSPGALGIE 120
Db 61 ASRNSGLYNTFFKYDNCCTYLNPNVKGKVIADAQNITISQYACHQVAVTILWSPGALGIE 120
Qy 121 FLKGRVILEELKSEGRCQCOQLILKDPKQLNSFKRTGMSQPFNNMKFETDYFVKVVPF 180
Db 121 FLKGRVILEELKSEGRCQCOQLILKDPKQLNSFKRTGMSQPFNNMKFETDYFVKVVPF 180
Qy 181 PSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNISQHGSDMQVDFHAPHNFG 240
Db 181 PSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNISQHGSDMQVDFHAPHNFG 240
Qy 301 LKPVHSPWAGPIRAVAITVPLAVTISAFATLFTVWCRKQKQENIYSHLDEESSESTYTA 360
Db 301 LKPVHSPWAGPIRAVAITVPLAVTISAFATLFTVWCRKQKQENIYSHLDEESSESTYTA 360
Qy 361 LPRRLRPRKPVFLCYSSKQGNHNVVQCFCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 361 LPRRLRPRKPVFLCYSSKQGNHNVVQCFCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Qy 421 WVIQIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLROAKQ 480
Db 421 WVIQIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKLROAKQ 480
Qy 481 SSSAALSFIAVYDYSCEGDPVGLDILSTKYRLMDNLPQLCSHLHRDGLQPGQHTR 540
Db 481 SSSAALSFIAVYDYSCEGDPVGLDILSTKYRLMDNLPQLCSHLHRDGLQPGQHTR 540
Qy 541 QGSRNFRSKSGRSLYVAI CNMHQFIDEEDPDWFEKQFVPPHPPPLRYREPVLKFDGL 600
Db 541 QGSRNFRSKSGRSLYVAI CNMHQFIDEEDPDWFEKQFVPPHPPPLRYREPVLKFDGL 600
Qy 601 VLNDVMCKPGPESDFCLKVEAAVIGATGPADSOHESQHGGLDQDGEARPALDGSAALOPL 660
Db 601 VLNDVMCKPGPESDFCLKVEAAVIGATGPADSOHESQHGGLDQDGEARPALDGSAALOPL 660
Qy 661 LHTWKAGSPSPMDRSGIYDSSVPSSELSLPLMGLSLTDQETSLTESVSSSGLGEE 720
Db 661 LHTWKAGSPSPMDRSGIYDSSVPSSELSLPLMGLSLTDQETSLTESVSSSGLGEE 720
Qy 721 PPALPSKLLSSGSKADLGCRSYTDHAVAPL 753
Db 721 PPALPSKLLSSGSKADLGCRSYTDHAVAPL 753
RESULT 2
ABB07627
ID ABB07627 standard; protein; 753 AA.
XX AC ABB07627;
XX DT 20-MAY-2002 (first entry)
XX DE Human cytokine receptor, Zcytor18 variant sequence.
XX

KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 269 /label= T269M
FT /note= "wild-type Thr is replaced with Met"
FT Misc-difference 750 /label= V750A
FT /note= "wild-type Val is replaced with Ala"
XX
XX W0200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-US023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Kuestner RE, Gao Z;
XX WPI; 2002-217048/27.
XX N-PSDB; ABA95033, ABA95034.
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX
XX Disclosure; Page 94-98; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumour growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 variant amino acid sequence
SQ Sequence 753 AA;
Query Match 99.8%; Score 4003; DB 5; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MAPWLQCSVFTYNACLSQSLAAAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFTYNACLSQSLAAAGGSGRARGADTCGRWMAAARPRLCVANEGVGP 60
Qy 61 ASRNSGLYNTFFKYDNCCTYLNPNVKGKVIADAQNITISQYACHQVAVTILWSPGALGIE 120
Db 61 ASRNSGLYNTFFKYDNCCTYLNPNVKGKVIADAQNITISQYACHQVAVTILWSPGALGIE 120
Qy 121 FLKGRVILEELKSEGRCQCOQLILKDPKQLNSFKRTGMSQPFNNMKFETDYFVKVVPF 180
Db 121 FLKGRVILEELKSEGRCQCOQLILKDPKQLNSFKRTGMSQPFNNMKFETDYFVKVVPF 180
Qy 181 PSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNISQHGSDMQVDFHAPHNFG 240
Db 181 PSIKNESNYHPFFRTTRACDILLQPDNLACKPFKPRNLNISQHGSDMQVDFHAPHNFG 240
Qy 241 PRFFVLYKLKHEGPFKRTCKBQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300

Db 241 FRFFYLKHEGPFKKTKCQBOTTEMSTCLLQNVSPGDIIELVDDTNTTRKVMHYA 300
Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 360
Db 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 360
Qy 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGELFLVAVSAIAEKLROAKQ 480
Db 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGELFLVAVSAIAEKLROAKQ 480
Qy 481 SSSAALSKFIIVYFDYSCGDPVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTR 540
Db 481 SSSAALSKFIIVYFDYSCGDPVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTR 540
Qy 541 QGSRNRYFRSKGRSLYVAICNMEHQFIDEEPDMFEKQFVPHPPPLRYREPVLKFDGSL 600
Db 541 QGSRNRYFRSKGRSLYVAICNMEHQFIDEEPDMFEKQFVPHPPPLRYREPVLKFDGSL 600
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAALQPL 660
Db 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAALQPL 660
Qy 661 LHTVKGSPSDMPDRDSGIYDSSVPSSLSLPLMEGLSTDQTTSTSLTSVSSSGLGEE 720
Db 661 LHTVKGSPSDMPDRDSGIYDSSVPSSLSLPLMEGLSTDQTTSTSLTSVSSSGLGEE 720
Qy 721 PPALPSKLLSSGCKADLGCRSYTDELHAAVAPL 753
Db 721 PPALPSKLLSSGCKADLGCRSYTDELHAAVAPL 753

RESULT 3
ABB07628
ID ABB07628 standard; protein; 739 AA.
XX
AC ABB07628;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human cytokine receptor, Zcytor18 splice variant.
XX
KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
XX
OS Homo sapiens.
XX
PN WO200208259-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-US023253.
XX
PR 26-JUL-2000; 2000US-0220747P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kuestner RE, Gao 2;
XX
FI WPI; 2002-217048/27.
DR N-PSDB; ABA95035, ABA95036.
XX
PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX
PS Claim 1; Page 102-106; 119pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC also localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 splice variant
XX
SQ Sequence 739 AA;
Query Match 97.8%; Score 3925; DB 5; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFFTVNACLNGSQLAAAGGSGRARGADTCGRMKAAARPLCLVANEGVGP 60
Db 1 MAPWLQCSVFFTVNACLNGSQLAAAGGSGRARGADTCGRMKAAARPLCLVANEGVGP 60
Qy 61 ASRNSGLYNITFKYDNCCTTYLNPVGHKVIADAQNTISQYACHDOVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNITFKYDNCCTTYLNPVGHKVIADAQNTISQYACHDOVAVTILWSPGALGIE 106
Qy 121 FLKGRVILBELKSEGRQCOQLILKDPKOLNSSFKRTGMESOPFLNMKFETDYFVKVVPF 180
Db 107 FLKGRVILBELKSEGRQCOQLILKDPKOLNSSFKRTGMESOPFLNMKFETDYFVKVVPF 166
Qy 181 PSIKNESNYHPFPRTRACDLLLLQPDNLACPKFPKPNLNISQSGDMQVDFDHPHNF 240
Db 167 PSIKNESNYHPFPRTRACDLLLLQPDNLACPKFPKPNLNISQSGDMQVDFDHPHNF 226
Qy 241 FRFFYLKHEGPFKKTKCQBOTTEMSTCLLQNVSPGDIIELVDDTNTTRKVMHYA 300
Db 227 FRFFYLKHEGPFKKTKCQBOTTEMSTCLLQNVSPGDIIELVDDTNTTRKVMHYA 286
Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTA 346
Qy 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406
Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGELFLVAVSAIAEKLROAKQ 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGELFLVAVSAIAEKLROAKQ 466
Qy 481 SSSAALSKFIIVYFDYSCGDPVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTR 540
Db 467 SSSAALSKFIIVYFDYSCGDPVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTR 526
Qy 541 QGSRNRYFRSKGRSLYVAICNMEHQFIDEEPDMFEKQFVPHPPPLRYREPVLKFDGSL 600
Db 527 QGSRNRYFRSKGRSLYVAICNMEHQFIDEEPDMFEKQFVPHPPPLRYREPVLKFDGSL 586
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAALQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAAALQPL 646
Qy 661 LHTVKGSPSDMPDRDSGIYDSSVPSSLSLPLMEGLSTDQTTSTSLTSVSSSGLGEE 720
Db 647 LHTVKGSPSDMPDRDSGIYDSSVPSSLSLPLMEGLSTDQTTSTSLTSVSSSGLGEE 706
Qy 721 PPALPSKLLSSGCKADLGCRSYTDELHAAVAPL 753
Db 707 PPALPSKLLSSGCKADLGCRSYTDELHAAVAPL 739

KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutcin.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 363

XX /label= Ser, Thr, Ala, Cys

XX WO200168859-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-US008678.

XX 16-MAR-2000; 2000US-0189816P.

XX 28-NOV-2000; 2000US-00724460.

XX (AMGE-) AMGEN INC.

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Db 47 ASRNSGLYNTFYDNCITTLNPFVGRHVIADAQNITISQYACHDQVAVTILWSPGALGIE 106
 QY 121 FLKGRVILBELKSEGRCQCOOLIKDPKQNLNSFKRTGMSQPLNKKFETDYFKVVPF 180
 Db 107 FLKGRVILBELKSEGRCQCOOLIKDPKQNLNSFKRTGMSQPLNKKFETDYFKVVPF 166
 QY 181 PSIKNESNYHPFFRTRACDLLOPDNLACKPFWKPRNLNISQHGSDMQVSDHAPNFG 240
 Db 167 PSIKNESNYHPFFRTRACDLLOPDNLACKPFWKPRNLNISQHGSDMQVSDHAPNFG 226
 QY 241 FRFFYLHYKLKHGPPFKRTCKQEQTTTSCLLQNVSPGDYIIELVDDTNTTKVHYA 300
 Db 227 FRFFYLHYKLKHGPPFKRTCKQEQTTTSCLLQNVSPGDYIIELVDDTNTTKVHYA 286
 QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTAA 360
 Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDESSSESTYTAA 346
 QY 361 LPRERLRPRPKVFLCYSSKDGQNHMVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
 Db 347 LPRERLRPRPKVFLCYSSKDGQNHMVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406
 QY 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELELVAVSAIAEKLROAKQ 480
 Db 407 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELELVAVSAIAEKLROAKQ 466
 QY 481 SSSAALSKEFTAVFYDSCGDVPGILDLSTKYRLMDNLPLCSSLHSHRDHGLQBPQHTR 540
 Db 467 SSSAALSKEFTAVFYDSCGDVPGILDLSTKYRLMDNLPLCSSLHSHRDHGLQBPQHTR 526
 QY 541 QGSRNRYFRSKGRSLYVAICNMHQFIDEPPDWEKQFVPPHPPPLRYREPVLPKPSGL 600
 Db 527 QGSRNRYFRSKGRSLYVAICNMHQFIDEPPDWEKQFVPPHPPPLRYREPVLPKPSGL 586
 QY 601 VLNDVMCKPGESDFCLKVEAAVLGATPADSOHESQHGGLDQGEARPALDGSAALOPL 660
 Db 587 VLNDVMCKPGESDFCLKVEAAVLGATPADSOHESQHGGLDQGEARPALDGSAALOPL 646
 QY 661 LHTVKGSPDMPRDSGYIDSSVSPSSLSLPLMEGLSTDQETSLTESVSSSSGLGBEE 720
 Db 647 LHTVKGSPDMPRDSGYIDSSVSPSSLSLPLMEGLSTDQETSLTESVSSSSGLGBEE 706
 QY 721 PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 752
 Db 707 PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 738

RESULT 6
 AAU09954
 ID AAU09954 standard; protein; 738 AA.
 XX
 AC AAU09954;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
 XX
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutcin.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 374
 FT /label= Val, Ile, Met, Leu, Phe, Ala, Nle

Query Match 97.1%; Score 3897; DB 4; Length 738;

Best Local Similarity 97.5%; Pred. No. 0;

Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFTVNAQLNGSLQVLAAGSGRAGADTCGRMKAAAPRLCVANEGVGP 60

Db 1 MAPWLQCSVFTVNAQLNGSLQVLAAGSGRAGADTCGRMKAAAPRLCVANEGVGP 46

QY 61 ASRNSGLYNTFYDNCITTLNPFVGRHVIADAQNITISQYACHDQVAVTILWSPGALGIE 120

[illegible]

CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 23
XX
SQ Sequence 738 AA;

Query Match 97.0%; Score 3894; DB 4; Length 738;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFTVNAACNGSOLAVAGSGRARGADTCGRWMAAARPRCLCVANEGVGP 60
Db 1 MAPWLQCSVFTVNAACNGSOLAVAGSGRARGADTCGRWMAAARPRCLCVANEGVGP 60

Qy 61 ASRNSGLYNIYFKYDNCNTYLPVCKHVIADQNIITISQYACHDOVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNIYFKYDNCNTYLPVCKHVIADQNIITISQYACHDOVAVTILWSPGALGIE 106

Qy 121 FLKGFVRLLEBKSGRQCQQLIKDPKQLNSSFKRTGMSQPFLLMKFFETDYFKVVPF 180
Db 107 FLKGFVRLLEBKSGRQCQQLIKDPKQLNSSFKRTGMSQPFLLMKFFETDYFKVVPF 166

Qy 181 PSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKPRNLNISQSGSDMQVSDFDHAPNFG 240
Db 167 PSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKPRNLNISQSGSDMQVSDFDHAPNFG 226

Qy 241 FRPFYLYKLKHGEPFKRKTQEQTTTSCLLQNVSPGDIYIELVDDTNTTKRWVHYA 300
Db 227 FRPFYLYKLKHGEPFKRKTQEQTTTSCLLQNVSPGDIYIELVDDTNTTKRWVHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQNMNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQNMNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 VWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELEFLAVASATAEKLROAKQ 480
Db 407 VWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELEFLAVASATAEKLROAKQ 466

Qy 481 SSSAALSXFIAYVPDYSCEGDVPGTLDLSTKYRLMDNLPQLCSHLSDHGLQEPGQTR 540
Db 467 SSSAALSXFIAYVPDYSCEGDVPGTLDLSTKYRLMDNLPQLCSHLSDHGLQEPGQTR 526

Qy 541 QGSRNRYFRSKSGRSLYVAICNMHQFIDEEPDPWFEKQFVPPHPPRLRYREPVLKFDGSL 600
Db 527 QGSRNRYFRSKSGRSLYVAICNMHQFIDEEPDPWFEKQFVPPHPPRLRYREPVLKFDGSL 586

Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSPQHSQHGGLDQDGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSPQHSQHGGLDQDGEARPALDGSAAQPL 646

Qy 661 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTSSVSSSSGLGEE 720

Db 647 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTSSVSSSSGLGEE 706

Qy 721 PPALPSKLLSGGCKADLGRSYTDELHAVAP 752

Db 707 PPALPSKLLSGGCKADLGRSYTDELHAVAP 738

RESULT 10
AAU09957
ID AAU09957 standard; protein; 738 AA.
XX
AC AAU09957;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #7.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 602 /label= Cys, Ala, Ser
FT
FT
FN WO200168959-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008678.
XX
XX 16-MAR-2000; 2000US-0189816P.
PR 28-NOV-2000; 2000US-00724460.
XX
XX (AMGE-) AMGEN INC.
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XX Jing S;
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX
XX Claim 24; Page; 159pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and

CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 24
XX
SQ Sequence 738 AA;

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|-----------------------|-----------------|--|------------|-------------|
| Query Match | 96.9%; | Score 3890; | DB 4; | Length 738; |
| Best Local Similarity | 97.5%; | Pred. No. 0; | | |
| Matches 733; | Conservative 1; | Mismatches 4; | Indels 14; | Gaps 1; |
| Qy | 1 | MAPWLQCSVFTTNACLSGOLAVAGGSGRARGADTCGRMKAAARPRCLCVANEGVGP | 60 | |
| Db | 1 | MAPWLQCSVFTTNACLSGOLAVAGGSGRANGVTCGR-----GVGP | 46 | |
| Qy | 61 | ASRNSGLYNTFFKYDNCCTYLPVKGHVIADAQNITISQYACHDQVAVTILMSFGALGIE | 120 | |
| Db | 47 | ASRNSGLYNTFFKYDNCCTYLPVKGHVIADAQNITISQYACHDQVAVTILMSFGALGIE | 106 | |
| Qy | 121 | FLKGFVILEELKSEGRCCQOLILKDPKOLNSSFKRTGMSQPLNKKFETDYVKKVVPF | 180 | |
| Db | 107 | FLKGFVILEELKSEGRCCQOLILKDPKOLNSSFKRTGMSQPLNKKFETDYVKKVVPF | 166 | |
| Qy | 181 | PSIKNESNYHFFPRTTRACDLLLPDNLACKPFWKPRNLNISQHGSDMQVSFHDHAPNFG | 240 | |
| Db | 167 | PSIKNESNYHFFPRTTRACDLLLPDNLACKPFWKPRNLNISQHGSDMQVSFHDHAPNFG | 226 | |
| Qy | 241 | FRFFLYHKLKHEGPFKRTCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA | 300 | |
| Db | 227 | FRFFLYHKLKHEGPFKRTCKQQTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA | 286 | |
| Qy | 301 | LKPVHSDWAGIRAVATVPLVAVISAFTLFTWCRKKQENIYSHLDESSSESTYTAA | 360 | |
| Db | 287 | LKPVHSDWAGIRAVATVPLVAVISAFTLFTWCRKKQENIYSHLDESSSESTYTAA | 346 | |
| Qy | 361 | LPRRLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE | 420 | |
| Db | 347 | LPRRLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE | 406 | |
| Qy | 421 | WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRQAKQ | 480 | |
| Db | 407 | WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRQAKQ | 466 | |
| Qy | 481 | SSSAALSKFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRQAKQ | 540 | |
| Db | 467 | SSSAALSKFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRQAKQ | 526 | |
| Qy | 541 | QGSRRNTFRSKGSLVVAICNMHQFIDEEPDWFEKQFVPPHPLRYREPVLEKFPDGL | 600 | |
| Db | 527 | QGSRRNTFRSKGSLVVAICNMHQFIDEEPDWFEKQFVPPHPLRYREPVLEKFPDGL | 586 | |
| Qy | 601 | VLNDVMCKPGPESDFCLKVEAVLGGATGADPADSÖHESQHGGLDQDGGEARLPALDGSAAQLPL | 660 | |
| Db | 587 | VLNDVMCKPGPESDFCLKVEAVLGGATGADPADSÖHESQHGGLDQDGGEARLPALDGSAAQLPL | 646 | |
| Qy | 661 | LHTVAKGSPDMPRDSGIDYSSVPSSELPLMEGLSTDQTTSTSLTESVSSSSGLGEE | 720 | |
| Db | 647 | LHTVAKGSPDMPRDSGIDYSSVPSSELPLMEGLSTDQTTSTSLTESVSSSSGLGEE | 706 | |
| Qy | 721 | PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 752 | | |
| Db | 707 | PPALPSKLLSGSGCKADLCGRSYTDELHAVAP 738 | | |

ID AAU09955 standard; protein; 738 AA.
XX
AC AAU09955;
XX
XX 14-FEB-2002 (first entry)
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
XX
XX Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmologic;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mucin.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 385 /label= Cys, Ser, Ala
XX
XX WO200168859-A2.
XX
XX 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008678.
XX
XX 16-MAR-2000; 2000US-0189816P.
XX 28-NOV-2000; 2000US-00724460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX
XX Claim 22; Page; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity. Note: This sequence is not given in the
XX specification but is based on the human Interleukin 17 (IL-17) receptor
XX like protein sequence (AAU09904) and has been created according to

| | | |
|-----------|--|--|
| CC | information given in claim 22 | |
| XX | Sequence 738 AA; | |
| SQ | Query Match 96.9%; Score 3890; DB 4; Length 738; Best Local Similarity 97.5%; Pred. No. 0; Matches 733; Conservative 1; Mismatches 4; Indels 14; Gaps 1; | |
| QY | 1 MAPWLQCSVFTVNAACLSQAVAGGSGRARGADTCGWRMKAARPRLCVANEVGP 60 | |
| DB | 1 MAPWLQCSVFTVNAACLSQAVAGGSGRAGVDTGWR-----GVGP 46 | |
| QY | 61 ASRNSGLYNTFKYDNCCTYLNPKVGHVIAQAQNTTISQYACHDQVAVTILWSPGALGIE 120 | |
| DB | 47 ASRNSGLYNTFKYDNCCTYLNPKVGHVIAQAQNTTISQYACHDQVAVTILWSPGALGIE 106 | |
| QY | 121 FLKGRFVILEELKSEGROCCQQLIKDPKQLNSSPKRTGMSQPFLLMKFETDYFKVVPF 180 | |
| DB | 107 FLKGRFVILEELKSEGROCCQQLIKDPKQLNSSPKRTGMSQPFLLMKFETDYFKVVPF 166 | |
| QY | 181 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISOHSDMQVSDHAPHNFG 240 | |
| DB | 167 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISOHSDMQVSDHAPHNFG 226 | |
| QY | 241 FRFFYLHYKLKHGEPFKRKTCKEQOTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300 | |
| DB | 227 FRFFYLHYKLKHGEPFKRKTCKEQOTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286 | |
| QY | 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQKQENIYSHLDEESSESTYTAA 360 | |
| DB | 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQKQENIYSHLDEESSESTYTAA 346 | |
| QY | 361 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420 | |
| DB | 347 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406 | |
| QY | 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKKGGRSGKGEFLFVAVSAIAEKLRQAKQ 480 | |
| DB | 407 WVIQIHESQFIIVVCSKGMKYFVDKKNYKKGGRSGKGEFLFVAVSAIAEKLRQAKQ 466 | |
| QY | 481 SSSAALSXFIAYFYDYSCEGDPVGLDLSKYRLMDNLPQLCSHLHSDHGLQBPQHTR 540 | |
| DB | 467 SSSAALSXFIAYFYDYSCEGDPVGLDLSKYRLMDNLPQLCSHLHSDHGLQBPQHTR 526 | |
| QY | 541 QGSRNRYPRSGRSLYVAICNMHQFIDEEDPWFQKQVPPHPPRLRYREPVELEKFDGSL 600 | |
| DB | 527 QGSRNRYPRSGRSLYVAICNMHQFIDEEDPWFQKQVPPHPPRLRYREPVELEKFDGSL 586 | |
| QY | 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQLPL 660 | |
| DB | 587 VLNDVMCKPGPESDFCLKVEAPVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQLPL 646 | |
| QY | 661 LHTVAGSPSPDRSDGIYDSSVSPSELPLMEGLSTDTQETSSLTESVSSSSGLGEE 720 | |
| DB | 647 LHTVAGSPSPDRSDGIYDSSVSPSELPLMEGLSTDTQETSSLTESVSSSSGLGEE 706 | |
| QY | 721 PPALPSKLLSSGCKADLCGRSYTDELHNAVAP 752 | |
| DB | 707 PPALPSKLLSSGCKADLCGRSYTDELHNAVAP 738 | |
| RESULT 12 | | |
| AAU11355 | | |
| ID | AAU11355 standard; protein; 738 AA. | |
| XX | AAU11355; | |
| AC | AAU11355; | |
| XX | 26-MAR-2002 (first entry) | |
| DT | Human DNAX cytokine receptor subunit 8 (DCRS8) polypeptide. | |
| DE | Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; | |
| XX | Human; DNAX cytokine receptor subunit 8; DCRS8; phosphate labelling; | |
| KW | gene therapy; protein therapy; immunological disorder. | |

| | | |
|----|---|-------------------------|
| XX | Homo sapiens. | |
| OS | Key | Location/Qualifiers |
| PH | Misc-difference 25 | /label= Val |
| FT | FT | /note= "Encoded by GTN" |
| XX | WO200190358-A2. | |
| FN | 29-NOV-2001. | |
| PD | 23-MAY-2001; 2001WO-US016767. | |
| XX | 24-MAY-2000; 2000US-0206862P. | |
| PR | (SCHE) SCHERING CORP. | |
| XX | Gorman DM; | |
| PI | WPI; 2002-106198/14. | |
| XX | N-PSDB; AAS18134. | |
| DR | Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide | |
| XX | useful for detecting antibodies generated in response to presence of | |
| PT | increased protein levels or immunological disorders. | |
| PT | Claim 1; Page 25; 148pp; English. | |
| PS | The invention relates to primate and rodent DNAX cytokine receptor | |
| CC | subunit (DCRS) polypeptides and the polynucleotides encoding them. The | |
| CC | receptors, or their portions may be useful as phosphate labelling enzymes | |
| CC | to label general or specific substrates. The subunits may also be | |
| CC | functional immunogens to elicit recognising antibodies, or antigens | |
| CC | capable of binding antibodies. A combination, e.g., including a DCRS can | |
| CC | be used as an immunogen for the production of antisera or antibodies | |
| CC | capable of distinguishing between other cytokine receptor family members. | |
| CC | A purified DCRS can also be used as a reagent to detect antibodies | |
| CC | generated in response to the presence of elevated levels of expression, | |
| CC | or immunological disorders which lead to antibody production to the | |
| CC | endogenous receptor. This sequence represents the human DCRS8 polypeptide | |
| XX | Sequence 738 AA; | |
| SQ | Query Match 95.5%; Score 3830.5; DB 5; Length 738; Best Local Similarity 96.3%; Pred. No. 0; Matches 725; Conservative 2; Mismatches 11; Indels 15; Gaps 2; | |
| QY | 1 MAPWLQCSVFTVNAACLSQAVAGGSGRARGADTCGWRMKAARPRLCVANEVGP 60 | |
| DB | 1 MAPWLQCSVFTVNAACLSQAVAGGSGRAXGADTCW-----XGVGP 46 | |
| QY | 61 ASRNSGLYNTFKYDNCCTYLNPKVGHVIAQAQNTTISQYACHDQVAVTILWSPGALGIE 120 | |
| DB | 47 ASRNSGLYNTFKYDNCCTYLNPKVGHVIAQAQNTTISQYACHDQVAVTILWSPGALGIE 106 | |
| QY | 121 FLKGRFVILEELKSEGROCCQQLIKDPKQLNSSPKRTGMSQPFLLMKFETDYFKVVPF 180 | |
| DB | 107 FLKGRFVILEELKSEGROCCQQLIKDPKQLNSSPKRTGMSQPFLLMKFETDYFKVVPF 165 | |
| QY | 181 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISOHSDMQVSDHAPHNFG 240 | |
| DB | 166 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISOHSDMQVSDHAPHNFG 225 | |
| QY | 241 FRFFYLHYKLKHGEPFKRKTCKEQOTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300 | |
| DB | 226 FRFFYLHYKLKHGEPFKRKTCKEQOTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 285 | |
| QY | 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQKQENIYSHLDEESSESTYTAA 360 | |
| DB | 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQKQENIYSHLDEESSESTYTAA 345 | |
| QY | 361 LPRERLRPRPKVFLCYSSKDGQNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420 | |

|||||
346 LPRERLRPRKVFVLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 405
|||||
421 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGEFLFVAVSAIAEKLRAQK 480
|||||
406 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGEFLFVAVSAIAEKLRAQK 465
|||||
481 SSSAALSQFTAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHRDHCLOEPGQHTR 540
|||||
466 SSSAALSQFTAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHRDHCLOEPGQHTR 525
|||||
541 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPHPPPLRYRPPVLEKFDOSGL 600
|||||
526 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPHPPPLRYRPPVLEKFDOSGL 585
|||||
601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGSAAQPL 660
|||||
586 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGSAAQPL 645
|||||
661 LHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDOTETSSLTESVSSSGLGEE 720
|||||
646 LHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDOTETSSLTESVSSSGLGEE 705
|||||
721 PPALPSKLLSGSGCKADIGCRSYTDELHAVAPL 753
|||||
706 PPALPSKLLSGSGCKADIGCRSYTDELHAVAPL 738
|||||
RESULT 13
ADB65245
ID ADB65245 standard; protein; 728 AA.
XX
AC ADB65245;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone TESTI20046540.
XX
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
cell regeneration; membrane protein; signal transduction-related protein;
transcription-related protein; osteoporosis; neurological disease;
cancer; tumour.
XX
OS Homo sapiens.
XX
PN EP1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
Yanamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB63275.
XX
XX New polynucleotides and polypeptides, useful for developing a diagnostic
marker or medicines for regulation of their expression and activity, or
as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
from 1970 fully defined nucleotide sequences which encode novel
polypeptides. Also claimed is a polypeptide encoded by the polynucleotide

or its partial peptide, an antibody binding to the polypeptide or peptide
of the polynucleotide, immunologically assaying the polypeptide or
peptide of the polynucleotide by contacting the polypeptide or peptide
with the antibody of the encoded protein, and observing the binding
between the two, a transformant carrying the polynucleotide in an
expressible manner and an antisense polynucleotide. The oligonucleotide
is useful as a primer for synthesising the polynucleotide, or as a probe
for detecting the polynucleotide. The polynucleotides and encoded
proteins are useful as pharmaceutical agents and many disease-related
genes may be included in them, for developing a diagnostic marker or
medicines for regulation of their expression and activity, or as targets
of gene therapy. The genes are involved in tissue and/or cell
regeneration. Membrane proteins, signal transduction-related proteins,
transcription-related proteins, disease-related proteins and genes
encoding them can be used as indicators for diseases (e.g. osteoporosis,
neurological diseases, cancer, tumours. The cDNA may be used to regulate
the activity or expression of the encoded protein to treat diseases. The
sequence presented is a protein of the invention. Note: Some of the
sequence data for this patent is not represented in the printed
specification, but is based on sequence information supplied by the
European Patent Office.
XX
SQ Sequence 728 AA;
Query Match 92.4%; Score 3708; DB 7; Length 728;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 56 EGVGPASRNSGLYNITFKYDNCCTTYLNPVGKHVIADAQNTITISQYACHQDVAVTILMSPG 115
DB 31 QGVGPASRNSGLYNITFKYDNCCTTYLNPVGKHVIADAQNTITISQYACHQDVAVTILMSPG 90
QY 116 ALGIEFLKGRFVILEELKSGROCOQLILKDPQLNSSFKRTGMESQFPLNMKPFETDYFV 175
DB 91 ALGIEFLKGRFVILEELKSGROCOQLILKDPQLNSSFKRTGMESQFPLNMKPFETDYFV 150
QY 176 KVVPPFSIKNESYVHPFFTRACDILLQPDNLACKPFWKPRNLINISQHSQDMQVSPDHA 235
DB 151 KVVPPFSIKNESYVHPFFTRACDILLQPDNLACKPFWKPRNLINISQHSQDMQVSPDHA 210
QY 236 PHNFGFRFFYLHYKLKHEGPFKTKCKQEQETTETSCLLQNVSPGDYIILVDDTNTTRK 295
DB 211 PHNFGFRFFYLHYKLKHEGPFKTKCKQEQETTETSCLLQNVSPGDYIILVDDTNTTRK 270
QY 296 VMEYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQENIYSHLDESSSS 355
DB 271 VMEYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQENIYSHLDESSSS 330
QY 356 TYTAALPRERLRPRKVFVLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCR 415
DB 331 TYTAALPRERLRPRKVFVLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCR 390
QY 416 EGQREWVIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGEFLFVAVSAIAEKL 475
DB 391 EGQREWVIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGEFLFVAVSAIAEKL 450
QY 476 RQAKQSSAALSQFTAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHRDHCLOEP 535
DB 451 RQAKQSSAALSQFTAVFDYSCGDVPGILDSTKYRLMDNLPOLCSHLHRDHCLOEP 510
QY 536 QGHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPHPPPLRYRPPVLEK 595
DB 511 QGHTROGSRNRYFRSKGRSLYVAICNMHQFIDEEPWFKEQFVPHPPPLRYRPPVLEK 570
QY 596 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGS 655
DB 571 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQDGEARPALDGS 630
QY 656 ALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDOTETSSLTESVSSSSG 715
DB 631 ALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDOTETSSLTESVSSSSG 690
QY 716 LGBEEPPALPSKLLSGSGCKADIGCRSYTDELHAVAPL 753


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Db      691  LGEPEPALPSKLLSSGCKADLGRSYTDLHVAAPL 728
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ID      AAU04958 standard; protein; 728 AA.
AC      AAU04958;
XX      24-OCT-2001 (first entry)
XX      Human Interleukin 17 receptor, IL-17RH4.
XX      Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; PRO20026;
XX      DNA 154095-2998; systemic lupus erythematosus; rheumatoid arthritis;
XX      osteoarthritis; diabetes mellitus; allergic disease; asthma;
XX      demyelinating disease; degenerative cartilaginous disorder;
XX      transplantation associated disease.
XX      Homo sapiens.
XX      Key
FH      Location/Qualifiers
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FT      19..24
FT      /note= "N-myristoylation site"
FT      Modified-site
FT      31..34
FT      /note= "Asn is N-glycosylated"
FT      Modified-site
FT      38..41
FT      /note= "Asn is N-glycosylated"
FT      Modified-site
FT      56..59
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FT      Modified-site
FT      113..116
FT      /note= "Asn is N-glycosylated"
FT      Modified-site
FT      147..150
FT      /note= "Asn is N-glycosylated"
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FT      182..185
FT      /note= "Asn is N-glycosylated"
FT      Region
FT      232..235
FT      /note= "cAMP/GMP-dependent protein kinase phosphorylation
FT      site"
FT      Modified-site
FT      266..269
FT      /note= "Asn is N-glycosylated"
FT      Domain
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FT      /note= "Transmembrane domain"
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FT      Region
FT      416..424
FT      /note= "Tyrosine kinase phosphorylation site"
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FT      /note= "N-myristoylation site"
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FT      517..522
FT      /note= "N-myristoylation site"
FT      Region
FT      574..579
FT      /note= "N-myristoylation site"
FT      Region
FT      652..657
FT      /note= "N-myristoylation site"
FT      Region
FT      707..712
FT      /note= "N-myristoylation site"
XX      WO200146420-A2.
XX      28-JUN-2001.
XX      PD
XX      20-DEC-2000; 2000WO-US034956.
XX

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PR      23-DEC-1999; 99US-0172096P.
PR      30-DEC-1999; 99WO-US031274.
PR      11-JAN-2000; 2000US-0175481P.
PR      18-FEB-2000; 2000WO-US004341.
PR      02-MAR-2000; 2000WO-US005841.
PR      21-MAR-2000; 2000US-0191007P.
PR      21-MAR-2000; 2000WO-US007532.
PR      02-JUN-2000; 2000WO-US015264.
PR      22-JUN-2000; 2000US-0213807P.
PR      22-AUG-2000; 2000US-00644848.
PR      24-AUG-2000; 2000WO-US023328.
PR      24-OCT-2000; 2000US-0242837P.
PR      10-NOV-2000; 2000WO-US030873.
PR      28-NOV-2000; 2000US-0253646P.
PR      01-DEC-2000; 2000WO-US032678.
XX      (GETH ) GENENTECH INC.
XX      Chen J, Pilvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;
XX      Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandien RL;
XX      Watanabe CK, Williams PM, Wood WI, Yansura DG;
XX      WPI; 2001-451708/48.
XX      N-ESDB; AAS09517.
XX      Novel PRO polypeptides homologous to interleukin-17, useful for the
XX      diagnosis and treatment of immune related disease e.g. rheumatoid
XX      arthritis and diabetes.
XX      Claim 10; Fig 18; 188pp; English.
XX      The sequence is PRO20026 which is the human Interleukin 17 receptor, IL-
XX      17RH4, encoded by DNA 154095-2998. A composition containing ant/agonists
XX      to the PRO polypeptides or individual components are useful for treating
XX      a mammal with an immune related disease, e.g. systemic lupus
XX      erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
XX      arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
XX      inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
XX      sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
XX      thyroiditis, diabetes mellitus, immune-mediated renal disease, a
XX      demyelinating disease, an autoimmune or immune-mediated skin disease,
XX      contact dermatitis, an allergic disease e.g. food hypersensitivity,
XX      asthma, a transplantation associated disease, or a chronic inflammatory
XX      demyelinating polynuropathy. Treating a degenerative cartilaginous
XX      disorder comprises administering a PRO1031 or PRO1122 polypeptide
XX      agonist, or antagonist to the mammal. Numerous examples of the diseases
XX      and disorders are given in the specification
XX      SQ      Sequence 728 AA;
XX      Query Match      92.3%; Score 3703; DB 4; Length 728;
XX      Best Local Similarity 96.7%; Pred. No. 0;
XX      Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;
XX      QY      42  RMKAARPRLCVANE-GVGPARNSGLYNIITFKYDNCNTYLNPGKHVIADAQNTISQY 100
XX      Db      3  RASAGVPALFVSGEQGVGPASRNSGLYNIITFKYDNCNTYLNPGKHVIADAQNTISQY 62
XX      QY      101  ACHDQVAVTILWSPGALGIEFKGFRVILELKGEGRCQCOQLIKDPKOLNSSFKRTGWE 160
XX      Db      63  ACHDQVAVTILWSPGALGIEFKGFRVILELKGEGRCQCOQLIKDPKOLNSSFKRTGWE 122
XX      QY      161  SQPFLNMKFETDYFKVVVPPFSIKNESNYHFFFRTRACDLLLOPDNLACKPFKWPRLN 220
XX      Db      123  SQPFLNMKFETDYFKVVVPPFSIKNESNYHFFFRTRACDLLLOPDNLACKPFKWPRLN 182
XX      QY      221  ISQ-----HGSDMQVSDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQT 267
XX      Db      183  ISQHGSDMQVSDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQT 242
XX      QY      268  ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 327
XX      Db      243  EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 302

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Perfect score: 4013
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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|------------|-------|-------------|--------|----|--------------------------------------|
| 1 | 3703 | 92.3 | 728 | 4 | US-09-747-259-18 Sequence 18, Appl |
| 2 | 3703 | 92.3 | 728 | 4 | US-09-816-744-18 Sequence 18, Appl |
| 3 | 312 | 7.8 | 866 | 2 | US-08-620-694A-10 Sequence 10, Appl |
| 4 | 312 | 7.8 | 866 | 3 | US-09-022-255-10 Sequence 10, Appl |
| 5 | 312 | 7.8 | 866 | 3 | US-09-022-696-10 Sequence 10, Appl |
| 6 | 312 | 7.8 | 866 | 3 | US-08-978-773-4 Sequence 4, Appl |
| 7 | 312 | 7.8 | 866 | 3 | US-09-022-253-10 Sequence 10, Appl |
| 8 | 312 | 7.8 | 866 | 3 | US-09-022-260-10 Sequence 10, Appl |
| 9 | 312 | 7.8 | 866 | 3 | US-09-022-259-10 Sequence 10, Appl |
| 10 | 312 | 7.8 | 866 | 3 | US-09-022-257-10 Sequence 10, Appl |
| 11 | 312 | 7.8 | 866 | 4 | US-09-549-679-10 Sequence 10, Appl |
| 12 | 312 | 7.8 | 866 | 4 | US-10-033-522-1 Sequence 1, Appl |
| 13 | 306 | 7.6 | 864 | 2 | US-08-620-694A-2 Sequence 2, Appl |
| 14 | 306 | 7.6 | 864 | 3 | US-09-022-255-2 Sequence 2, Appl |
| 15 | 306 | 7.6 | 864 | 3 | US-09-022-696-2 Sequence 2, Appl |
| 16 | 306 | 7.6 | 864 | 3 | US-08-978-773-2 Sequence 2, Appl |
| 17 | 306 | 7.6 | 864 | 3 | US-09-022-253-2 Sequence 2, Appl |
| 18 | 306 | 7.6 | 864 | 3 | US-09-022-260-2 Sequence 2, Appl |
| 19 | 306 | 7.6 | 864 | 3 | US-09-022-259-2 Sequence 2, Appl |
| 20 | 306 | 7.6 | 864 | 3 | US-09-022-257-2 Sequence 2, Appl |
| 21 | 306 | 7.6 | 864 | 4 | US-09-549-679-2 Sequence 106, App |
| 22 | 135.5 | 3.4 | 385 | 4 | US-09-598-360B-106 Sequence 12, Appl |
| 23 | 135.5 | 3.4 | 502 | 4 | US-09-747-259-18 Sequence 12, Appl |
| 24 | 135.5 | 3.4 | 502 | 4 | US-09-816-744-12 Sequence 11658, A |
| 25 | 135.5 | 3.4 | 504 | 4 | US-09-949-016-11658 Sequence 1, Appl |
| 26 | 116.5 | 2.9 | 993 | 1 | US-08-348-143-1 Sequence 1, Appl |
| 27 | 116.5 | 2.9 | 993 | 1 | US-08-571-785-1 Sequence 1, Appl |

Sequence 1, Appli
Sequence 1, Appli
Sequence 8005, Ap
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 303, App
Sequence 303, App
Sequence 6384, Ap
Sequence 25826, A
Sequence 9916, Ap
Sequence 9917, Ap
Sequence 10562, A
Sequence 14749, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 664, App
Sequence 6898, Ap

ALIGNMENTS

RESULT 1

US-09-747-259-18
; Sequence 18, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Collin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24

;; PRIOR APPLICATION NUMBER: US 60/242,837
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: US 60/253,646
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 18
;; LENGTH: 728
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-747-259-18

Query Match 92.3%; Score 3703; DB 4; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMKAARPRLCVANE-GVGPSARNISGLYNTFFKYDNCCTTYLNPVGHVIAADAQNITISQY 100
DB 3 RASASGVPALFVSGEQGVGPSARNISGLYNTFFKYDNCCTTYLNPVGHVIAADAQNITISQY 62

QY 101 ACHDQAVATILWSFGALGIEFLKGFVRVILELSEKSGRQCQOLILKDPKQLNSSPFRGTME 160
DB 63 ACHDQAVATILWSFGALGIEFLKGFVRVILELSEKSGRQCQOLILKDPKQLNSSPFRGTME 122

QY 161 SQPLNNKFTDYFVKVVPFPIKNSNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 220
DB 123 SQPLNNKFTDYFVKVVPFPIKNSNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 182

QY 221 ISQ-----HGSMDQVDFDHPNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 267
DB 183 ISQHGSMDQVDFDHPNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 242

QY 268 ETTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 243 EMTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

QY 328 ATLFTVMCRKKQENIYSHLDDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 387
DB 303 ATLFTVMCRKKQENIYSHLDDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 362

QY 388 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKK 447
DB 363 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKK 422

QY 448 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSAALSFKFIAYVFDYSCGEGDVPGLD 507
DB 423 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSAALSFKFIAYVFDYSCGEGDVPGLD 482

QY 508 LSTKYRLMDNLPOLCSHLHSDHGLQBPQHTQGRSRRNYFRSKSGRSLYVAICNMHQFI 567
DB 483 LSTKYRLMDNLPOLCSHLHSDHGLQBPQHTQGRSRRNYFRSKSGRSLYVAICNMHQFI 542

QY 568 DEEDPWPEKQVFPHPPLRYREPVLKFDISGLVNDVMCKPGPESDFCLKVEAAVLGAT 627
DB 543 DEEDPWPEKQVFPHPPLRYREPVLKFDISGLVNDVMCKPGPESDFCLKVEAAVLGAT 602

QY 628 GPADSQHESQHGGLDQGEARPALDGSAAQLPHTLVKAGSPDMPRDSGIYDSSVPSSE 687
DB 603 GPADSQHESQHGGLDQGEARPALDGSAAQLPHTLVKAGSPDMPRDSGIYDSSVPSSE 662

QY 688 LSLFLMEGLSDQTETSLTSVSSSGGLGEEPPALPSKLLSSGSKADLGCRSYTDEL 747
DB 663 LSLFLMEGLSDQTETSLTSVSSSGGLGEEPPALPSKLLSSGSKADLGCRSYTDEL 722

QY 748 HAVAPL 753
DB 723 HAVAPL 728

RESULT 2

US-09-816-744-18
;; Sequence 18, Application US/09816744
;; Patent No. 6579520
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Jian
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul
;; APPLICANT: Grimaldi, Christopher
;; APPLICANT: Gurney, Austin
;; APPLICANT: Li, Hanzhong
;; APPLICANT: Hillan, Kenneth
;; APPLICANT: Tumas, Daniel
;; APPLICANT: VanLookeren, Menno
;; APPLICANT: Vandlen, Richard
;; APPLICANT: Watanabe, Colin
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William
;; APPLICANT: Yansura, Daniel
;; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;; FILE REFERENCE: PI381R1C1P2(US)
;; CURRENT APPLICATION NUMBER: US/09/816,744
;; CURRENT FILING DATE: 2001-03-22
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 18
;; LENGTH: 728
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-816-744-18

Query Match 92.3%; Score 3703; DB 4; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMKAARPRLCVANE-GVGPSARNISGLYNTFFKYDNCCTTYLNPVGHVIAADAQNITISQY 100
DB 3 RASASGVPALFVSGEQGVGPSARNISGLYNTFFKYDNCCTTYLNPVGHVIAADAQNITISQY 62

QY 101 ACHDQAVATILWSFGALGIEFLKGFVRVILELSEKSGRQCQOLILKDPKQLNSSPFRGTME 160
DB 63 ACHDQAVATILWSFGALGIEFLKGFVRVILELSEKSGRQCQOLILKDPKQLNSSPFRGTME 122

QY 161 SQPLNNKFTDYFVKVVPFPIKNSNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 220
DB 123 SQPLNNKFTDYFVKVVPFPIKNSNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 182

QY 221 ISQ-----HGSMDQVDFDHPNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 267
DB 183 ISQHGSMDQVDFDHPNFGFRFFVLYHKLKHEGPFKRKTCQSQTT 242

QY 268 ETTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
DB 243 EMTSCLLQNVSPGDIYIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

QY 328 ATLFTVMCRKKQENIYSHLDDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 387
DB 303 ATLFTVMCRKKQENIYSHLDDESSSTYTAALPRERLRPRPKVFLCYSSKQGNHNV 362

QY 388 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKK 447
DB 363 VOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKK 422

QY 448 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSAALSFKFIAYVFDYSCGEGDVPGLD 507
DB 423 NYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSAALSFKFIAYVFDYSCGEGDVPGLD 482

QY 508 LSTKYRLMDNLPOLCSHLHSDHGLQBPQHTQGRSRRNYFRSKSGRSLYVAICNMHQFI 567
DB 483 LSTKYRLMDNLPOLCSHLHSDHGLQBPQHTQGRSRRNYFRSKSGRSLYVAICNMHQFI 542

QY 568 DEEDPWPEKQVFPHPPLRYREPVLKFDISGLVNDVMCKPGPESDFCLKVEAAVLGAT 627

Db 543 DEEDWFEKQVPPHPPPLRYREPVLKFDGSLVNDVMCKGPGSDPCLKVEAAVLGAT 602
Qy 628 GPADSQHSQGGLDQDGEARPALDGSAAOPLHTVKAGSPDMPRDSGIYDSSVPSSE 687
Db 603 GPADSQHSQGGLDQDGEARPALDGSAAOPLHTVKAGSPDMPRDSGIYDSSVPSSE 662
Qy 688 LSLPLMEGLSTDQETSTSLTSVSSSSGIGREEPPALPSKLLSSGCKADIGCRSYTDEL 747
Db 663 LSLPLMEGLSTDQETSTSLTSVSSSSGIGREEPPALPSKLLSSGCKADIGCRSYTDEL 722
Qy 748 HAVAPL 753
Db 723 HAVAPL 728

RESULT 3
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)597-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-620-694A-10

Query Match 7.8%; Score 312; DB 2; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
Qy 69 NITFKYDNC--TYYLNPVGKHVIADAQNIT-----ISOYACHDQ-----VAVTILWS 113
Db 49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLPFPVAHIEWT 99

Qy 114 -PGALGIEFLKGRFVILIEELKSEGRQCOQLILKDPKOLNSFKRTGMSOPFLNMKETD 172
Db 100 LQTDASILYLEGAELSVLQLTNRLCVR--FEFLSKLRHHRRWRRTFSHFV--VDPDQE 156
Qy 173 YFVKV--VPFPIKSNESYHPFFERTRACDLLLQPDNLACK--PFWKPRNL----- 219
Db 157 YEVTVHLPKPIPDGPNHOSKNFLVPDCEHARKVTTTPCMSSGSLWDP-NITVETLEAH 215
Qy 220 -----NISQHGSDMOVSFDHAPHNFGFRFFYLHYLKLKHEGFFRKCTCKQEQTTETT 270
Db 216 QLRVSFTLWNSTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEFHQRSNVLTLLNLK 274
Qy 271 SCLLQNVSPGDYIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVLSAF 327
Db 275 GCCRHHQVQIOFFFSCLNCLRHSAVSCPEMPDTPPEIPDYMPFLWYFWFTGTSILLVG 334
Qy 328 ATLFTVMCRKKQKQENIYSHLDESSSESTVTAALPRERLRPRP-----KVFLCYSKDQCN 383
Db 335 SVILLIVCMTWRLAGPGS---EKYSDDTKTDTGLPAADLPPPLKPKRWIIYSA-DHPL 390
Qy 384 HMYVQCFAFYFLQDFCGCEVALDLMEDFSLCREQREWV---TQKIHESOFIIVVCSKG 439
Db 391 YVDVLKFAQFLLTACCTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
Qy 440 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLROAKQSSSAALSKEFIA 491
Db 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDGLFTAAVMNMLPDFKR-----PACFGTVV 501
Qy 492 VYF--DYSCGDVPGILDSTKYRLMDNLPOLCSHLHSRDHGLQBPQGHTRQG---SRRNYF 548
Db 502 CYFSEVSCDGDVPLFGAAPRYPLMDRFEV--YFRIQDLEMFQFGRHVRVGEISGDNYL 559
Qy 549 RSKSGRSLYVAICNMHOFIDEEPWF-----KQFVPPHPPPLRYREPVLEKFDGSL 600
Db 560 RSPGGRQIRALDRFRDMQVRCPDWFECENLYSADDQDAPSLDEEV-FEELPLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----SQHGG 640
Db 618 VKRAPLVRE-PGSOACLAIDPLVGEEGAAVAKLEPHLQPRGQAPAPQLHTLVLAEEGA 676
Qy 641 LDQDGEARPALDGSAA--ALQ-----PLLHTVKAGSPDMPRDSGIYDSSVPSSESLP 691
Db 677 LVAAVEFGPLADGAAVRLALAGEGEACPLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 692 LMEGLSTDQETSTSLTSVSSSSGIGREEPPALPSKLLSSGCKADLGC 740
Db 728 L--GSSPTMASPDLLPEDVR-----EHLEGLMLSLPEQSLSCQAQGGC 768

RESULT 4
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255

220 -----NISGSDMQVSDHAPNFGFRFFYLHYLKLKHEGFFKRTCKOBTETT 270
216 QLRVSFTLWNESTHYQILLTSFPHWNSCFEWHM-HI PAPRPEFHORSNVTLRLNK 274
271 SCLLQNVSPGDIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVLSAF 327
275 GCCHQVQIOFPFSSCLNCLRHSAIVSCPEMPDTPPIPYMPLWVYFVITGISILLVG 334
328 ATLFTVMCRKQOENIYSHLDESESSSTYTAALPRERLRPP---KVFLCYSSKDQON 383
335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSA-DHPL 390
384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQEWV---IQKHESQFIIVVCSKG 439
391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCRSG 450
440 MKYFVDKKNYKHGGG-----RSGKGGLFLVAVSAIAEKLRQAKQSSAALSKEFIA 491
451 TR-----AKWQALLGKGPVRLRCDHGXKPVGDLFTAAMNMILPDKR-----PACFGTVV 501
492 VYF-DYCEGDPVPGILDSTKYRLMDNLPQLCSHLHSDHGLQBPQGHTRQG--SRRNYF 548
502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGEISGNYL 559
549 RSKGSRSLYVAICNMHOFIDEEPWFE-----KQFVPPHPPPLRYREPVLKFDGSL 600
560 RSPGGRQLRAALDRFDWQVRCDFWECENIYSADDQDAPSLDEEV-FEEPLLP-GTGI 617
601 VLNDVMCKPGPESDFCLKVAAVLGATGPADSQHE-----SOHGG 640
618 VKRAPLVRE-PGSQACLAIDPLVGEAGAAVAKLEPHLQPRGQAPQPLHVLAAEBA 676
641 LDQGEARPALDGA---ALQ-----PLLHTVAGSPSDMPRDSIGIYDSSVPSSELSLP 691
677 LVAAVEPGLADGAARLALAGEACPLLSGPGAG-----RNSVLF--LPVDPEDSP 727
692 LMEGLSTDTQTTSSITSVSSSGSGLEGEPPALPSKLLSSGCKADLGC 740
728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 6

US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Trout, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,773
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-4

Query Match 7.8%; Score 312; DB 3; Length 866;
Best Local Similarity 23.4%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 69 NITFYKDNQ--TTVLNPVGRHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 113
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSPKDLQIQLHFAHTQGDLPVVAHLEWT 99
QY 114 -PGALGIEFLKGRFVILEELKSEGRQCOQLIKDPKOLNSFKRTGMESQPFLLNMKFTD 172
Db 100 LQTDASLTYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDQE 156
QY 173 YFVKV--VPPPSIKNESNYHPFFRTRACDILLQPDNLACK--PFWKPRNL-----219
Db 157 YEVTVHRLPKPIPDGDPNHQSKNPLVDPDCEHARMKVTTPCMSSGSLMDP-NITVETLEAH 215
QY 220 -----NISGSDMQVSDHAPNFGFRFFYLHYLKLKHEGFFKRTCKOBTETT 270
Db 216 QLRVSFTLWNESTHYQILLTSFPHWNSCFEWHM-HI PAPRPEFHORSNVTLRLNK 274
QY 271 SCLLQNVSPGDIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVLSAF 327
Db 275 GCCHQVQIOFPFSSCLNCLRHSAIVSCPEMPDTPPIPYMPLWVYFVITGISILLVG 334
QY 328 ATLFTVMCRKQOENIYSHLDESESSSTYTAALPRERLRPP---KVFLCYSSKDQON 383
Db 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSA-DHPL 390
QY 384 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQEWV---IQKHESQFIIVVCSKG 439
Db 391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCRSG 450
QY 440 MKYFVDKKNYKHGGG-----RSGKGGLFLVAVSAIAEKLRQAKQSSAALSKEFIA 491
Db 451 TR-----AKWQALLGKGPVRLRCDHGXKPVGDLFTAAMNMILPDKR-----PACFGTVV 501
QY 492 VYF-DYCEGDPVPGILDSTKYRLMDNLPQLCSHLHSDHGLQBPQGHTRQG--SRRNYF 548
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGEISGNYL 559
QY 549 RSKGSRSLYVAICNMHOFIDEEPWFE-----KQFVPPHPPPLRYREPVLKFDGSL 600
Db 560 RSPGGRQLRAALDRFDWQVRCDFWECENIYSADDQDAPSLDEEV-FEEPLLP-GTGI 617
QY 601 VLNDVMCKPGPESDFCLKVAAVLGATGPADSQHE-----SOHGG 640
Db 618 VKRAPLVRE-PGSQACLAIDPLVGEAGAAVAKLEPHLQPRGQAPQPLHVLAAEBA 676
QY 641 LDQGEARPALDGA---ALQ-----PLLHTVAGSPSDMPRDSIGIYDSSVPSSELSLP 691
Db 677 LVAAVEPGLADGAARLALAGEACPLLSGPGAG-----RNSVLF--LPVDPEDSP 727
QY 692 LMEGLSTDTQTTSSITSVSSSGSGLEGEPPALPSKLLSSGCKADLGC 740
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 7

US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305

us-10-717-282-2.ra

TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17

Db 451 TR-----AKWALLGKAPVRLRCDHGRKPVGDLFTAAMNMLPDKFR-----PACFGYV 501
Qy 492 VYF-DYSCGVDVPGILDSTKYRLMDNLPOICSHLHSDHGLQEPGQHTROG--SRNYF 548
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 549 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYRBPVLEKFDGSL 600
Db 560 RSPGGRQLRAALDRFRDQWVRCPDWFECEENYSADDDQAPSLDEEV-FEPLLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSHE-----SOHGG 640
Db 618 VKRAPLVRE-PSQACLAIDPLVGEEGAATAKLEPHLQPRGQAPQPLHTLVLAEEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLLHTVKAGSPDMPRDSGIYDSVPSSELSLP 691
Db 677 LVAAVEGPLADGAARVLALAGEACPLLGSPGAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQETSTSLTESVSSSSGLGEEPPALPSKLLSGSCKADI/GC 740
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 10

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-257-10

Query Match 7.8%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
Qy 69 NITFKYDNC--TTYLNPVGRKHVADIQAQNT-----ISOYACHDQ-----NAVITLMS 113
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWT 99
Qy 114 -PGALGIEFLKGRVILEELKSGRCQOQILILDPKQLNSSFRTKGNESQFFLNMKETD 172
Db 100 LQTDASILYLEGAEALSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFHFV-VDPQE 156
Qy 173 YFVKV--VPFSPKSNHYHFFFRTRACDLLLLQPNLACK--PFWKPRNL-----219
Db 157 YEIVVHLPKPIPDGPNHQSCKNLPDCEHARKVTTTCMSSGSLWDP-NITVETLEAH 215
Qy 220 -----NISQHSQDMQVSDPHAPNFGFRFFLYHLKHBGPPFRKTKCQOBTETT 270
Db 216 QLRVSTFLWNETHYQILLTSFFHMHNSCFEHHM-HIPAPRPEEFHQRNSVTLTLRLNK 274
Qy 271 SCLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVLSAF 327
Db 275 GCCRHQVQIQIFFSSCLNCLRHSAVSCPEMPTPEPIPDYMLPWYWFITGISILVG 334
Qy 328 ATLFTVMCRKKQENIYSHLDESSSSTVTAALPRERLRPR-----KVFLCYSSKDGQN 383
Db 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPKRWIIISA-DHPL 390
Qy 384 HMNVQCFAYFLQDFCGCEVALDWMEDFSLCREGQREW----IQKIHESQFIIVVCSKG 439
Db 391 YVDVLKFAQFLLTAGCTEVALDLLEBQAISEAGVMTWVGROKQEMVESNKIIVLCRG 450
Qy 440 MKYFVDKQNYKHGGG-----RSGKGEFLVAVSAIAEKLROAKQSSSAALSFA 491
Db 451 TR-----AKWALLGKAPVRLRCDHGRKPVGDLFTAAMNMLPDKFR-----PACFGYV 501
Qy 492 VYF-DYSCGVDVPGILDSTKYRLMDNLPOICSHLHSDHGLQEPGQHTROG--SRNYF 548
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 549 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYRBPVLEKFDGSL 600
Db 560 RSPGGRQLRAALDRFRDQWVRCPDWFECEENYSADDDQAPSLDEEV-FEPLLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSHE-----SOHGG 640
Db 618 VKRAPLVRE-PSQACLAIDPLVGEEGAATAKLEPHLQPRGQAPQPLHTLVLAEEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLLHTVKAGSPDMPRDSGIYDSVPSSELSLP 691
Db 677 LVAAVEGPLADGAARVLALAGEACPLLGSPGAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQETSTSLTESVSSSSGLGEEPPALPSKLLSGSCKADI/GC 740
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 11

US-09-549-679-10
; Sequence 10, Application US/09549679
; Patent No. 6680057

; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; Spriggs, Melanie
; Fanslow, William
; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,679
FILING DATE: 14-Apr-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-549-679-10

Query Match 7.8%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
69 NITPKYDNC--TYYLNPVKGHVIADAQNI-----ISQYACHDQ-----VAVTILWS 113
49 NCTVKNSTCLDDSWIHP-----RNLTSSPKDLQIQLHFAHTQQGDLFPVAHIWT 99
114 -PGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSSFKRTGMSQFLNMKFTD 172
100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRWRFTFSHFV-VDPDQE 156
173 YFVKV--VPPFSIKNESNYHFFRTRACDILLQPDNLACK---PFWKPRNL-----219
157 YEVTVHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTPPCMSGSLWDP-NITVETLEAH 215
220 -----NLSQSGDMQVSDHAPHNFGFRFFYLHYKLHKGFPKRTCKQEQTETT 270
216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEFHQSRNVTLRLNLK 274
271 SCLLNQVSPGYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
275 GCCRHOVQIQPFSSCLNDCLRHSAVSCEMPDTPPEIPDYMWPLWYVFWFITGISILVG 334
328 ATLFTVMCRKQOENIYSHLDESESTYTAALPRELRPRP-----KVFLCYSSKQGN 383
335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMYIYSA-DHPL 390
384 HNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGQEWV---IQKHESQFIIVVCSKG 439
391 YVDVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWVGKQKQEWESNSKIIVLCISRG 450
440 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLQAKQSSAALSFKFTA 491
451 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYV 501
492 VYF-DYSCGDPVPGILDSTKTYRLMDNLPOLCSHLHSRDHGLQEPGQHTROG--SRNYF 548
502 CYFSEVSCDGVPLDFAAPRYPLMDRFEV--YFRIQDLEMFQPGRMHVRVSGELSDNYL 559
549 RSKGRSLYVAICNHHQFIDEEDPWF-----KQFVFPHPPLRYREPVLKFDSCGL 600

Db 560 RSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADDDQAPSLDEEV-FEPELPLPP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHE-----SOHGG 640
Db 618 VKRAPLVRE-PGSOACLAIDPLVGEEGAATAVAKLEPHLQPRGQAPQPLHTLVLAEBEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLAHTVKAGSPSDMPRDSGIYDSSVRSSELSLP 691
Db 677 LVAAVEFGPLADGAARVRLALAGEGACPLIGSPGAG-----RNSVLJF---LPVDPEDSP 727
Qy 692 LMEGLSTDQETSTSLTESVSSSGLEGEPPALPSPKLLSSGSKADLGC 740
Db 728 L--GSSTFPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGC 768
RESULT 12
US-10-033-522-1
Sequence 1, Application US/10033522
Patent No. 6793919
GENERAL INFORMATION:
APPLICANT: MOHLER, Kendall M.
TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
FILE REFERENCE: 2982-A
CURRENT APPLICATION NUMBER: US/10/033,522
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,230
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 866
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-522-1

Query Match 7.8%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 3.8e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
69 NITPKYDNC--TYYLNPVKGHVIADAQNI-----ISQYACHDQ-----VAVTILWS 113
49 NCTVKNSTCLDDSWIHP-----RNLTSSPKDLQIQLHFAHTQQGDLFPVAHIWT 99
114 -PGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSSFKRTGMSQFLNMKFTD 172
100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRWRFTFSHFV-VDPDQE 156
173 YFVKV--VPPFSIKNESNYHFFRTRACDILLQPDNLACK---PFWKPRNL-----219
157 YEVTVHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTPPCMSGSLWDP-NITVETLEAH 215
220 -----NLSQSGDMQVSDHAPHNFGFRFFYLHYKLHKGFPKRTCKQEQTETT 270
216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEFHQSRNVTLRLNLK 274
271 SCLLNQVSPGYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 327
275 GCCRHOVQIQPFSSCLNDCLRHSAVSCEMPDTPPEIPDYMWPLWYVFWFITGISILVG 334
328 ATLFTVMCRKQOENIYSHLDESESTYTAALPRELRPRP-----KVFLCYSSKQGN 383
335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKVMYIYSA-DHPL 390
384 HNVVQCFAFYFLQDFCGCEVALDLWEDFSLCREGQEWV---IQKHESQFIIVVCSKG 439
391 YVDVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWVGKQKQEWESNSKIIVLCISRG 450
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451 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYV 501
492 VYF-DYSCGDPVPGILDSTKTYRLMDNLPOLCSHLHSRDHGLQEPGQHTROG--SRNYF 548

Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 549 RSKGSRSLYVAICNMHOFIDEEPWFE-----KQFVPPHPPPLRYREPVLEKFDPSGL 600
Db 560 RSPGGRQJRALDRFRDMQVRCDFWCEGENYSADDOAPSLDEEV--FEEPLLP-GTGI 617
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHE-----SQHGG 640
Db 618 VKRAPLVRE-PSGQACLAIDLPLVGEAGAAVAKLEPHLQPRGPAPQPLHTLVLAABEGA 676
Qy 641 LDQGEARPALDGA---ALQ-----PLLHTVKAQSPDMRPSGIDYSSVPSLSLP 691
Db 677 LVAAVEPGPLADGAARLALAGEAGEACPILGSPGAG-----RNSVLF--LPVDPEDSP 727
Qy 692 LMEGLSTDQITSTSLTESVSSSGLGREEPPALSKLLSGSCKADLGC 740
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 13

US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-620-694A-2
Query Match 7.6%; Score 306; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
Qy 40 GWRM-----KAAARPREL-----CVANEGVGPSARNSGLYNITFKYDNCCTVYLNPGK 86

Db 17 GWLLLLNLVLAAPGRASPRLLDFPAPVCAQEGSLCRVKNSTCLDDSWIHPKNTLTPSSPKNI 76
Qy 87 HVTADAQNIITISQYACHDQAVT-ILWS-FCALGIEELKGFVILEELKSEGRCCQ--- 141
Db 77 YI-----NLSVSTQHGELVPVLHVEWTLOTDSILYLEGAELSVLQINTNERLCVXPQF 131
Qy 142 --LILKDPKOLNSFKRTGMESQPFLLNMKFETDYFVKVPFPSPKINSESNYHPFFRTRAC 199
Db 132 LSMLOHHRKWRFSF-----SHFVDPGQGEYEVTVHHLKPIPDGDPNKHSLIFVPDC 185
Qy 200 D---LLLQPNLACKPFWKPRNLI---SQH-----GSDMQV 230
Db 186 EDSMKMTTSCVSSGSLWDP-NITVETLDTQHLRVDFTLWNESTPYOVLLSFSDSENHS 244
Qy 231 SFD-----HAPNFGFRFFYLHYKLKHE---GPFKRKTKCQEQTTTTCLL 274
Db 245 CFDVVKQIFAPRQEFHQANVTTLKFKWCCHHVQVQPF--FSSCLND-----CLR 296
Qy 275 QNVSPGDYIITELVDDTNTTRKVMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
Db 297 HAVTVCPVI-----SNVT-----VPKPVADYIPLWYGLITLIAL---LLVGSVIVL 341
Qy 331 FTVMCRKKQENIYSHLDEESSESTYTAALPRERLRPRKPVFLCYSSKQGNHNVQC 390
Db 342 IICMTWELSGADQEKHGDDSKINGILPVALDITPPPLRPR-KWIVYSA-DHPLYVEVVLK 399
Qy 391 FAYFLQDFCGCEVALDLWEDFSLCREGQREWVTK-----IHESQFIIVVCSKGNKYFVDK 446
Db 400 FAQFLITACGTEVALDLLEBQVISEVGVMTWVSQRKQEMVESNSKIILCSRG-----TQ 454
Qy 447 KNYKHGG-----GRSGKGELFLVAVSAIAEKLRQAKQSSAALSKEFTAVYFDY 496
Db 455 AKWKAILGWAEPVAVQLRCDHWKPGADLFTAMNWLIPDKR-----PACFTYVVCYFSG 509
Qy 497 SC-EGDVPGLDLSKYRLMDNLPLQCSHLHSDRHGLQEPGQ--HTROGSRNRYFRSKSG 553
Db 510 ICSERDVPDLFNITSRYPFLMDRFEV--YFRIQDLEMFQGRMHRVRELTDGNYLQSPSG 567
Qy 554 RSLYVAICNMHOFIDEEPWFQFVFFHP-----PPLR---YREPVLKEDSGVLANDVM 606
Db 568 ROLKEAVLRFQEWQTCQDFWFERENCLADGQDLPSLDEEVFEDPLLP--GGGIVKQOPL 626
Qy 607 CKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQD-----GEAR 648
Db 627 VRELPSDGLVVDVCV-----SEESRMAKLDPQLWFPQRELVAHTLQSMVLPARQV 677
Qy 649 PALDGSAAQLPLHTVKAGSPSDMP--RDS-----GIYDSSV---FSSLSLPL----- 692
Db 678 PA---AHVVEPLHLPDGSGAAALPMTEDSEACPILGVQRNSILCLPVDSDDLPLCSTPM 734
Qy 693 -----MEGLSTDQITSTSLTESVSSSGLGEEEEPP-----ALPSKLLSSGCKADLG 739
Db 735 MSPDLQGDAREQLESLMLSVLQOQSLSGPLESWPRPEVVLGCTPSEEBQQRQSQSDQ 794

RESULT 14
US-09-022-255-2
; Sequence 2, Application US/0902255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match 7.6%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;

QY 40 GWRM-----KAAARPRL-----CVANEGVGPASRNSGLYNITFKYDNCCTTYLNPVGK 86
DB 17 GWLLLLLVNAPGRASPLDFFAPVCAQEGSLCRVKNSTCLDSDSWHPKNTLTPSSPKNI 76
QY 87 HVIADAQNITISQVACHDOQAVT-ILMS-PCALGIEFLKGRVRLBELKSGRCQQ---141
DB 77 YI-----NLSVSTQHGLVPLVHVEWTQDASILYLEGAELSVLQNTNRLCVKRFQF 131
QY 142 --LILKPKQLNSGFKRTGMSQPLNKKFTDIFVKVPPPSKNSNYHPPFRTRAC 199
DB 132 LSLMLQHHRKWRFSF-----SHFVVDPGQYEVTVVHHLPKPIPDGDPNHSKIIFVPDC 185
QY 200 D---LLLPQDNLACKPFKPRNLNI-----SQH-----GSDMQV 230
DB 186 EDSKMKMTTSCVSGSLMDP-NITVETLDTQHLRVDFTLWNESTPYQVLLSFSDSENHS 244
QY 231 SFD-----HAPHNFGFRFFYLHYKLKHE---GPFKRKTCKQEQTETTSCLL 274
DB 245 CFDDVVKQIFAPRQEFHQANVTFLSKFHCCHHVQVQPF-FSSCLND-----CLR 296
QY 275 QNVSPGDYIELVDNTTRKVMHVALPV--HSP-WA-GPIRAVAITVPLVISAFAYL 330
DB 297 HAVTVPCSVI-----SNTT-----VPRPVADYIPLWYGLITLIAI-----LLVGSVIVL 341
QY 331 FTWCRKQKQENIYSHLDEESSESTYTAALPRELRPRPKPVFLCYSSKSGQNHNVQC 390
DB 342 ICTWRLSGADQKXGDDSKINGLLPVADLTTPPLRPR-KWIVYSA-DHPLYEVVVLK 399
QY 391 PAYFLQDFCGCEVALDLWEDFSLCREQREWIQK-----IHESQFIIVVCSKGMKYFYDK 446
DB 400 FAQFLITACGTIEVALDLLEEQVISEVGMVTWVRQKQEWESNSKIILCSRQ-----TQ 454
QY 447 KNYKHKG-----GRSGKGELFLVAVSAIAEKLQAKQSSSAALESKFAIVFDY 496
DB 455 AKWKAILGWAEPAVQLRCDHWKPADGLFTAAMNMLLPDFKR-----PACFGTYVVCYFSG 509
QY 497 SC-EGDVFGILLDLSTKYRLMDNLPLQCSHLHSRDHGLQEPGQ--HTRQGSRRNYFRSKSG 553

510 ICSERDVPDLFNITSRYPLMDREFEV--YFRIQDLEMFEGRMHVRLELTGDNLYLQSPSG 567
554 RSLYVAICNMHQFIDBEPWFQKQFVPFHP-----PPLR-----YREPVLKEFDSGLVLDVDM 606
568 RQKEAVLRFQEWQTCQDFNFERENCLADQDLPSLDEEVFEDPLLP--GGGIVKQOPL 626
607 CKPGPESDFCLKYEAVALGATGPADSOHESQHGGLDOD-----GEAR 648
627 VRELPSDGLVVDVCV-----SEESRMALDPLQWLPQRELVAHTLQSMVLPAEQV 677
649 PALDGSAAQLOPLLHTVKAGSPSMP--RDS-----GIYDSSV---PSSLSLPL-----692
678 PA---AHVVEPLHLPDGSAAQLPMTEDSEACPLLGQVQRNSILCLPVDSDDLPLCLCTPM 734
693 -----MEGLSTDOTETSSLTESVSSSSGLCEEP-----ALPSKLLSSSSCKADLG 739
735 MSPDHLOGDAREQELSLMLSVLQOSSLGQPLESWPFEVLEGTPEERQSRQSVQSDQG 794

RESULT 15
US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 08/620,694
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-2

Query Match 7.6%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 1.6e-22;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;

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Qy 40 GWRM-----KAAAPREL-----CVANEGVGPASRNSGLYNTFKYDNCCTYLNVPVGK 86
Db 17 GWLLLLLNLVAPGRASRLLDFFAPVCAQEGLSCEVXNSCLDDSDWIHPKXLTFPSSPXNI 76
Qy 87 HVIADAQNITISQYACHDQAVT-ILMS-PCALGIEFLKGRFVLEBELKSEGRQCOQ---141
Db 77 YI-----NLSVSTQHGLVPLVHVEWTLQTDASILYLEGAELSVLQNTNERLCVKQFQF 131
Qy 142 --LILKDPKQLNSSFKRTMESQFPLNMKFETDYFVKVPPSPKXNSYHHPFFRTRAC 199
Db 132 LSQLQHRKRWRFSGF-----SHFVDPGQGEYEVTVHHLPKPIPDGDPNHKSKIIFVPCD 185
Qy 200 D---LLLPQDNLACKPFKPNLNI---SOH-----GSDMQV 230
Db 186 EDSKXKMTTSCVSGSLWDP-NITVELDTQHLRVDFTLWNSTPYQVILLESFSDSENHS 244
Qy 231 SFD-----HAPHNFGFRFFLYHKLKHE---GPPKRKCKQEQTETTTSCLL 274
Db 245 CFVVVKQIFAPRQEEFHQRANVTFTLSKFHWCHHHVQVQPF-FSSCLND-----CLR 296
Qy 275 QNVSPGDIYIELVDVDTTRKMHYALKPV--HSP-WA-GPIRAVAITVPLVVISAFATL 330
Db 297 HAVTVPCPVI-----SNTT-----VPKPVADYIPLWYGLITLIAI-----LLVGSVIVL 341
Qy 331 FTVNCRKKQENIYSHLDESSSESTVTAALPRERLRPRPKVPLCYSSKDGQNHMNVQOC 390
Db 342 IICMTWRLSGADQEKHGDDSKINGILPVADLTTPPLRPR-KWIVYSA-DHPLYVEVVLK 399
Qy 391 FAYFLQDFCGCEVALDWFSLCREGQREWVIOK----IHESQFIIVCCKGMYFVDK 446
Db 400 FAQLITACGTGEVALDLLEEQVISEVGVMTWVSRQKQEMVESNSKIILCSRG-----TQ 454
Qy 447 KNYKHGG-----GRSGHGELFLVAVSAIAEKLRQAKOSSSAALSKFTAVYFDY 496
Db 455 AKWKAIIIGWABPAVOLRCDHWKPAQDLFTAMNMILPDKR-----PACFTYVVCYFSG 509
Qy 497 SC-EGDVPGLDLSTKYRLMDNLPLCLSHLSRDHGLQEPQ--HTROGSRNRYFRSKSG 553
Db 510 ICSEKVPDLFNITRYPLMDRFEV--YFRIQLEMFEPGRMHVRELTDGNYLQSPSG 567
Qy 554 RSLYVAICNMHQFIDEBPDWFQKQFPFHP-----PPLR---YREPVLKFDGSLVLDVM 606
Db 568 RQLKEAVLRFQEWQTCQDFWFERENCLADGQDLPLSDEEVFEDPPLPP-GGIVKQOPL 626
Qy 607 CKPQESDFCLKVEAAVLGATGPADSQHSQHGGLDQD-----GEAR 648
Db 627 VRELFP-SDGCLVVDVCV-----SEESRMAKLDPLQWPQRELVAHTLQSMVLPAEQV 677
Qy 649 PALDGSAAALQPLLHTVKAGSPDMP--RDS-----GIYDSSV---PSSELSLPL-----692
Db 678 PA---AHVVEPLHLPDGSAAAQIPLMTEDSEACPILGVQRNSILCLPVDSDDLPLCSTPM 734
Qy 693 -----MEGLSTDQTTESLTSVESSSGGLGEEPP-----ALPSKLLSSGSKADLG 739
Db 735 MSPDHLQDAREQLESLMVLQSLGQPLESWPRPEVVLEGGCTPSEEEQORSQVQSDQG 794
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Search completed: August 9, 2005, 11:51:08
Job time : 42.7138 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:37:17 ; Search time 30.2019 Seconds
(without alignments)
2398.896 Million cell updates/sec

Title: US-10-717-282-2
Perfect score: 4013
Sequence: 1 MAPWLQCSVFPTVACLNG.....CKADLGCRSYDELHVAAPL 753

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 3005 | 74.9 | 564 | T42695 | hypothetical prote |
| 2 | 170.5 | 4.2 | 846 | T27282 | hypothetical prote |
| 3 | 126.5 | 3.2 | 718 | T30113 | hypothetical prote |
| 4 | 117 | 2.9 | 757 | T09081 | telomere-associate |
| 5 | 117 | 2.9 | 917 | T04661 | hypothetical prote |
| 6 | 117 | 2.9 | 2946 | T00867 | hypothetical prote |
| 7 | 116.5 | 2.9 | 901 | F83781 | transposase (08) / |
| 8 | 115.5 | 2.9 | 938 | I49071 | protein kinase - m |
| 9 | 115 | 2.9 | 998 | S37627 | protein-tyrosine k |
| 10 | 110 | 2.7 | 535 | T17212 | hypothetical prote |
| 11 | 110 | 2.7 | 592 | I49239 | vesicle transport |
| 12 | 108.5 | 2.7 | 3788 | T13960 | beige protein homo |
| 13 | 107.5 | 2.7 | 3942 | T42730 | Basoon protein - |
| 14 | 107 | 2.7 | 3788 | T30851 | lysosomal traffick |
| 15 | 106.5 | 2.7 | 638 | T24273 | protein F1504.27 [|
| 16 | 106 | 2.6 | 1448 | D86477 | Subtilase family p |
| 17 | 105 | 2.6 | 901 | JC5093 | dead ringer nuclea |
| 18 | 105 | 2.6 | 1571 | T14155 | zinc finger protei |
| 19 | 104 | 2.6 | 1462 | B36182 | protein-tyrosine-p |
| 20 | 103.5 | 2.6 | 663 | A39897 | GTPase-activating |
| 21 | 103.5 | 2.6 | 930 | A84668 | Argonaute (AGO1)-1 |
| 22 | 102 | 2.5 | 813 | B47485 | ABR protein 2 - hu |
| 23 | 102 | 2.5 | 859 | A49307 | 98K GTPase-activat |
| 24 | 101.5 | 2.5 | 822 | T47485 | ABR protein 1 - hu |
| 25 | 101.5 | 2.5 | 1639 | T50119 | probable sensory t |
| 26 | 101 | 2.5 | 641 | T05497 | hypothetical prote |
| 27 | 101 | 2.5 | 664 | T51247 | ARR2 protein limpo |
| 28 | 101 | 2.5 | 1275 | A38985 | nucleotide exchang |
| 29 | 100.5 | 2.5 | 938 | T05533 | hypothetical prote |

ALIGNMENTS

RESULT 1

T42695
hypothetical protein DKFp434N1928.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T42695

R:Bloecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22230

A:Accession: T42695

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-564 <AAA>

A:Cross-references: UNIPROT:Q9UFA0; EMBL:AL133097

A:Experimental source: adult testis; clone DKFp434N1928

C:Genetics:

A:Note: DKFp434N1928.1

Query Match 74.9%; Score 3005; DB 2; Length 564;

Best Local Similarity 99.8%; Pred. No. 1.9e-232;

Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 190 | HPFFRTRACDLLLQPDNLACKPFWKPNLNISQHGSDMQVSFDHAPNFGRFFYLHYK | 249 |
| Db | 1 | HPFFRTRACDLLLQPDNLACKPFWKPNLNISQHGSDMQVSFDHAPNFGRFFYLHYK | 60 |
| Qy | 250 | LKHEGPFKRKTKCKQEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPA | 309 |
| Db | 61 | LKHEGPFKRKTKCKQEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPA | 120 |
| Qy | 310 | GPIRAVAITVPLVVISAFATLFTWCRKQENIYSHLDESSSTYTALPRRLRPR | 369 |
| Db | 121 | GPIRAVAITVPLVVISAFATLFTWCRKQENIYSHLDESSSTYTALPRRLRPR | 180 |
| Qy | 370 | PKVFLCYSSKQGNHNMVQCFAFLQDFCGCEVALDLWEDFSLCREGQREWVIQKHES | 429 |
| Db | 191 | PKVFLCYSSKQGNHNMVQCFAFLQDFCGCEVALDLWEDFSLCREGQREWVIQKHES | 240 |
| Qy | 430 | QPIIIVVCSKGMKYFVDKKNYKHGGGRSGKGFELVAVSAIAEKLRQAKQSSSAALSXF | 489 |
| Db | 241 | QPIIIVVCSKGMKYFVDKKNYKHGGGRSGKGFELVAVSAIAEKLRQAKQSSSAALSXF | 300 |
| Qy | 490 | IADVFDYCEGDPVIGILDSTKYRLMDNLPOLCSHLHSDHGLQPGQGHTRQGSRRNFR | 549 |
| Db | 301 | IADVFDYCEGDPVIGILDSTKYRLMDNLPOLCSHLHSDHGLQPGQGHTRQGSRRNFR | 360 |
| Qy | 550 | SKSGRSLVVAICNMHQFDEEPPDMFEKQFVPHPPPLRYREPVLEKFGSLVNDVMCKP | 609 |
| Db | 361 | SKSGRSLVVAICNMHQFDEEPPDMFEKQFVPHPPPLRYREPVLEKFGSLVNDVMCKP | 420 |
| Qy | 610 | GPESDFCLKVEAAVLGATGPADSQHESQHGGLDQGEARPALDGSAAALQPLLHTYKAGSP | 669 |

A>Note: F8D20.70
C:Superfamily: Arabidopsis thaliana hypothetical protein F8D20.70

| | | | | |
|-----------------------|-------------------|-----------------|-------------|-------------|
| Query Match | 2.9%; | Score 117; | DB 2; | Length 917; |
| Best Local Similarity | 18.3%; | Pred. No. 0.84; | | |
| Matches 167; | Conservative 130; | Mismatches 296; | Indels 320; | Gaps 42; |

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QY 19 NGSQLAVAGGSRARGATTCGRM---KAAAPR---LCVANEGV-----58
DB 92 NGRSVS-----GYSNG-DILWSIPSKGECSPESAMCKNLGYKSEKIPIASLKWVY 145

QY 59 --GPASR-----NSGLYNITTFKYDNTCTYLNVPVKHV---IADAQNI---TISQYACHDQ 105
DB 146 AEGKASRVVYIGSSNSLQVLLNEQTETRMIKGLHVSPECADMEMI IADVNEQSKHKQ 205

QY 106 VAVTILWSPGALGI---EFLKGFVIIIEELKSEGRQCQOLIKDPKQLNSSFKRTGMSQP 163
DB 206 DFLFVLGKGRVAYDDYMIKYLIOQSKSSPSLPKETVVKLFPFSDSSITVGKFLITNP 265

QY 164 --FLANKFETDY-----FVKVVPFPIKNEKN---YHPFF-----FRTRACDILLQPD 206
DB 266 SHULNLSDE-DYAAQLAKDAVPFFPHTVPKSSSAHFPGFTVKVKVYIITCHDGIISW 324

QY 207 NLACK-----PFWKPR-NLNIISQHG-----SDMQVSEDFHAPNFGFRFFYLHY 248
DB 325 DMTCSPIILVLFKEIQDQDVSSRGNAALTALHYDINSRLLVSGDHNGMVLRYRKFPEPY 384

QY 249 KLKH-----EGPKPR-----KTCKEQTTTTSCLLQNVSP-----GDYIIELV 287
DB 385 LTENSPIFPQGLKGNHIVQSVKVIKLTGSIITQKSNKHLAIGSQDGHDSLVEVI 444

QY 288 DDNTTRKVMHYALKVHSPWAGPIRAVAITVPLVVISAFATLFT-----332
DB 445 D-----ALTPLY-----LQVSLVDIEEANVLYTKHIASDICPGIISLQ 482

QY 333 -----YMKRKKQOENITYSHLDESSSSTYTAALPRELRAPRPKVFCLYCSKD 380
DB 483 FESCIVQGFKNVIVNMRDSSVFA-LDSDTGNMIGTNMKPK-----KPKVLYMQILD 536

QY 381 GQNHMNVQCFAYFLQDFQCEVALDLWEDFSLCREGQREWVITQKIHESQIIVVCS---437
DB 537 GK-----QDTSG-----NGFDTSRES-----TWEEISIROPSPVLVCSEKA 571

QY 438 -----KGMKYFVDKKNYKHKG-----GGRGSGKGEFLVAVSAIAE-----K 474
DB 572 IYIYSLAHVVQGVKVLHKKKFSPPICSASTFYGTSGVG---LTLVTTDGTVEIRSLPE 628

QY 475 LRAQKQS-----SSAALSFTAVFDYCEGD-----VPGILDLSLTKYRLMD 516
DB 629 LSQKQTSIRGFTYSSPKPNSLPEITISASWDGDLVMVNGDDELIVSSVLPPQKETRLVE 688

QY 517 NLPQLCSHLSDRHGLQEPQCHTRQGSRR-----NYFRSKGSRSLYVAICNMHQFIDEE 570
DB 689 SM---NRVYKONSVCHEGIITSSSPREKKSMPGSVFKTQSKRTTDTPESSKETIEEL 744

QY 571 PDWPEKQFVFP-----HPPPLRYREPVLEKFPDS 598
DB 745 SKIFSTANFPNNNNVENSREINTITRVEDEBELDIDDIDDDHHNPOOQOEKPKQGGILS 804

QY 599 GL-----VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSOHGGL-----641
DB 805 GLSKQKQWNRFPNPKGLKQMAAKNEKSVV-----TNDEKHEKNKGAIVDQIKKYGFTSS 860

QY 642 DQDGEARPALDGAALQPLLHTVKAGSPSDMPRDSGIYDYSVPSSLSLPLMEGLSTDOT 701
DB 861 DENGAAKWA-----QSKLQD-----NLKKLGIGISLRTT 888

QY 702 ETSSLTESVSSSS 714
DB 889 EMEDTAKSFSSSTA 901
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RESULT 6


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Db 559 RCFWDSPEFIKSDGQVASFALFD--KLRRGEGENMIEVIDLSKTYRNQVW-----KGIN 612
Qy 442 YFVDKKNYKHGGGSGKGLFLVAVSAI-----AEKLRQAKSSAALSK 488
Db 613 MFIEKGEMVGLLPGNAGKSTTSMISLIQPTSGDVLIIKGGSIHKSKAIRSILGVVPPQ 672
Qy 489 FIAYFYDSC-----GDVPGIIDLSTKYRLMDNLPLQCSHLHSRDLHGLOPEQOHTRQ 542
Db 673 EIAYHDLTARENLAFFGKIYGLKEELKXR--MESTLQV-----GLEE-----RQN 718
Qy 543 SRRNYFRSKGRSLYVAICNNHQ---FIDEEP 571
Db 719 DRVHTFGMKRRRLNIAVALLHEPELIIMDEP 750

RESULT 8
149071
protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49071
R:Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A:Title: Identification of novel protein kinases expressed in the myocardium of the deve
A:Reference number: 149071; MUID:95200798; PMID:7893599
A:Accession: I49071
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-938 <RES>
A:Cross-references: UNIPROT:Q60669; EMBL:U11493; NID:G595418; PIDN:AAA67925.1; PID:G5954
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:571-839/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif
F:862-928/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115.5; DB 2; Length 938;
Best Local Similarity 19.4%; Pred. No. 1.1; Mismatches 285; Indels 259; Gaps 45;
Matches 160; Conservative 120;

Qy 9 SVFFTVNACL-NGSOLAVA-----AGGSGR---ARGADTCGWRMKAARPRLC----- 52
Db 170 SILVAPRACIANAEVSVPLKLYCNGDGEWVPVVGACTCATGHEPAKESQCRACPPGSY 229
Qy 53 VANEGVGPA-----SRNSG-----LYNTFFKYN-----CTTYLNPVGVKHVIADAQ 93
Db 230 KAKQEGPCLPCCPNRSRTTSPAASICTCHNNFYRADSDSADSACTTRSP-PRGVISNV- 287
Qy 94 NITISQYACHQVAVTILWS-PGALGIEFLKGFVRVILELK-SEG-----ROCOQLIL 144
Db 288 -----NETSLILEWSEPRDLGRRDILLYNYICKKRGSSGAGGATCSRCDNVE 337
Qy 145 KDPQLNSSFKRTGMESQPFNLKMFETDYFKVAVPFPSPISKNESNYHPPFFRTRACDILLQ 204
Db 338 FVPRLGLTERVHIS-----HLLAHTRYTEVQAVGVGSKPLPPRYAAVNTTNOAA 392
Qy 205 PDNLACKPFWKPRNLNISOHGSMDQVSDHAPHNFGFRFFYLHYLKHGEPF-KRKTCKQ 263
Db 393 PSEV-----PTLHSHSTSGSSLLTSWAPPRNG-----VILDYEMKY---FEKSKAAS 439
Qy 264 EOTTETTSCLQNVSPP-GDYIIELVDDTNTTKV-----MHYALKPVHSPWAGPIRAVA 316
Db 440 TVTSQKNSVQLDGLQPDARYVQVQ-----RARTVAGYQYTHPAEFETTSSRSGAQQLQ 494
Qy 317 ITVPLVVI SAFA-----TLFTVMCKKQENIYSHLDESSSTYTAAALPERLRP 368
Db 495 EQLPLIVGNSVAGFVFMVVVVVIAVCLRKORH-----GPDABYTEKL-QOYIAP 543
Qy 369 RPKVFLCYSSKDGQNMNVVOCFAFYFLQDFC-GCEVALDLMEDFSLCREGOREWVIQIH 427
Db 544 GKMVVIDFTYEDPN-EAVREFAKEIDVSCVKIEVIGAGEFGEVCR----- 589
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Qy 428 ESQFIIVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAI-----AEKLRQAKOSS 483
Db 590 -----GRLKLPGRREVFA-VAIKTLKVGYTERQRDRFSEA 623
Qy 484 AALSKEFIADVYDSCGDPVGIIDLS---TKYR-----LMDNLPLQCSHLHSRDLHGLO 533
Db 624 SNNGQF-----DHENIIRLEGVVTYKSPVPMILLTEFMENC-ALDSFLRLND----- 667
Qy 534 EPQOHT-----RQSSRRNY-FRSKSGRSLYV---AIC-----NNHQFIDE 569
Db 668 --GQFTVIQLVGLMGLGIAAGMKYLSMNVYVHRDLAARNILVNSNLVCKVSDFGLSRLEF 725
Qy 570 EPDWFKEQF-----VPEH---PPPLRYREPVLKEDS-----GLVLDNVMCKGPE 612
Db 726 DPS--DPTTSSLGKIPIRWTAPEIAYR-----KFDASDVMSYGVIMWEVMS----- 773
Qy 613 SDFCLKVEAAVLGATGAPDASQHSQHGLDQDGEARALDGSAAALQPLLLHTVKAGSPSDM 672
Db 774 -----YGEQFYWNMSNQDDINAVEQDRLPPEMDCPTALHQLMASCWVRDRLNR 822
Qy 673 PRDSGIYD-----SSVPSSELSLPLMEGLSTDQ 701
Db 823 PKFSQIWNITLDKLIRNAASLKVTASAPSG-MSQPLLDRTVPDYT 865

RESULT 9
S37627
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37627
R:Boehme, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Strebhardt, K.; Ruebs
Oncogene 8, 2857-2862, 1993
A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
A:Reference number: S37627; MUID:93390963; PMID:8337371
A:Accession: S37627
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-998 <BOE>
A:Cross-references: UNIPROT:P54753; EMBL:X75208; NID:9406867; PIDN:CAA53021.1; PID:94068
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki
F:631-899/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:922-988/Domain: SAM homology <SAM>

Query Match 2.9%; Score 115; DB 2; Length 998;
Best Local Similarity 19.0%; Pred. No. 1.4;
Matches 158; Conservative 122; Mismatches 301; Indels 250; Gaps 42;

Qy 35 GADTCGWRMKAARPRLC-----VANEGVGPA-----SRNSG-----LYNTFFK 73
Db 267 GACTCATGHEPAKESQCRPCPGSYKAKQEGPCLPCCPNRSRTTSPAASICTCHNFPYR 326
Qy 74 YDN-----CTTYLNPVGVKHVIADAQNTISQYACHQVAVTILWS-PGALGIEFLKGF 126
Db 327 ADSASDASACTTVSP-PRGVISNV-----NETSLILEWSEPRDLGVRDLDLYN 374
Qy 127 VILEELKSEG-----ROCOQLILKDPQLNSSFKRTGMESQPFNLKMFETDYFKVAVPFP 181
Db 375 VICKKCHGAGGASACSRCDNVEFVPRQLGLSEPRVHTS-----HLLAHTRYTEVQAVN 429
Qy 182 SIKNESNYHPPFFRTRACDILLQPDNLACKPFWKPRNLNISOHGSMDQVSDHAPHNFGP 241
Db 430 GVSQKSLPPRYAAVNTTNOAASEV-----PTLHSHSSGSSLLTSWAPPRNG- 481
Qy 242 RFFYLHYLKHGEPF-KRKTCKQOQTETTSCLQNVSPP-GDYIIELVDDTNTTKVMHY 299
Db 482 --VILDYEMKY---FEKSEGIASITVSQMSNVQLDGLRDPARYVQVQ-----RARTVAGY 531
Qy 300 A--LKPVH-----SPWAGPIRAVAITVPLVVISAFATL-----FTVMCKKQENIYS 345
Db 532 QOYSRPAEFETTSSRSGAQQLQEQPLIVGSAATAGLVFVAVVAVVIAVCLRKORH----- 587
```


R;Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
A;Accession: T13960
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3788 <MOR>
A;Cross-references: UNIPROT:Q922X9; EMBL:AB020019; NID:dl035670; PID:dl035670; PIDN:BA43
A;Experimental source: strain DA; spleen
C;Genetics:
A;Gene: beige

Query Match 2.7%; Score 108.5; DB 2; Length 3788;
Best Local Similarity 19.4%; Pred. No. 33;
Matches 144; Conservative 98; Mismatches 267; Indels 235; Gaps 38;
Qy 20 GSQLAAGSGRARGADTCGRMKAAARPRLCVANEGVGVPASRNSGLYNITPKYDNCCT 79
Db 651 GETLQGLCGAGPCGLPSPSYR-----QGILP-----SSSEDFLWKWDALAE 695
Qy 80 YLNPVGKHVIADAQNIITISOVACH--DQVAVILWSPGALGIEFLKGRFVILEELKSEG- 136
Db 696 YQNFIFOE--DRLHTQIASHCNLIQKGNVIVQ-----KLYNIFNPVLQGV 743
Qy 137 ---RQCQILKDPKQLNSFKRTGMSQPLNKKFT-DYFVKVP-----FP 181
Db 744 ELVHCQQLSI-----TSAQTHMSSQLKQYLPQEVLIQIYKLTPLILLKSRVIRDLFL 795
Qy 182 SIKN-----ESNY-----HPP-FRTACDLLLOPNLACKPFWKPRNLNISOHGSDMQ 229
Db 796 SCNGVNHIELNYLDGIRSHLSKAFETLIVSLGQQKRAAVPGV---DGLDIOQLSSLS 852
Qy 230 VSPDHAPHNFGFRFFLYHLKHEGPPKRTCKQBTETTSCLLQNVSPGDYIIELVDD 289
Db 853 V-----GPSLHK-----QQASTDPCSRLK-----FYASLRDT 880
Qy 290 TMTTRKVNHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTVWCKRKKQOENIYSHLDE 349
Db 881 DPKKRKTVHQ-----DAHINTINLFCVAF-----LCVSKAEDSDRESAN- 920
Qy 350 ESSSSTY--TAALPRRLRPKPVFLCYSSKDGQNHVV-----OCFAYFLQDFCGCEV 403
Db 921 ESEDTSGYDSTASEPLSHMLPRLSL-----ENVVLPSPCELIH----- 958
Qy 404 ALDLWEDFSLCREGRENW--IQTHESQFI-----IVVCSKGMKYFVDKKNYKKGGRG 457
Db 959 AADTW---SMCK-----WYMLNSVFOQFHRLGQFQVCHB-LIFMIQKLFHRTEDQG 1009
Qy 458 SGKELF-----LVAVSAIAEKLRQAKQSSAALSKEFIAYVFDYSCEDGVPGLD----- 507
Db 1010 RQGEMSVNKGQGLMRIIOPEMILKEDYSSSTAPEPGFLKKSADRVSELESQHMLPTSAB 1069
Qy 508 --LSTK-----YRLMDNLPLQCSH-----LHSRDHGLQEPGQHTROG 542
Db 1070 QILATKSPGAKTPMNOESETCLQSIIRLESLLAICLHSARASQKMELELPSQ----- 1124
Qy 543 SRNRYFRSKSGSLVACNMHQFIDEP-----DWFEKQFVFPFPPPLRYREP 591
Db 1125 -----SLSENILCELDHLSQSKVAETELAKPLFDALLKVALGNHSAIDLPGDT 1174
Qy 592 VLEKFDGLVLDNMCKPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646
Db 1175 VTEKSHPS---EVLVSQPGDFSEAEEDSQCSLKLGLGEEGYEADSESNPEDGETQDDGV 1231
Qy 647 ARPALDG--SAALQOP--LLHTVKAG 667
Db 1232 ELPEAEGFSGSVIPNNLLESLTHG 1255

Query Match 2.7%; Score 107.5; DB 2; Length 3942;
Best Local Similarity 19.1%; Pred. No. 43;
Matches 58; Conservative 29; Mismatches 99; Indels 117; Gaps 11;
Qy 516 DNLPLCASHLSRDHGLQEPGQHTROGSRNRYFRSKSGSLYVAIC-----NMHQFIDEE 570
Db 3535 DTCFQFCS-----SHSMPDVQEHVKDGPRAHYKREEGYMLDDSHCVVVSSEAYHLGOEE 3589
Qy 571 PDMEKQFVFPFPPPLRYRE-----PVLEKF-----DSGLVLDNMCKPKG 610
Db 3590 TDMFDK---PRDARSDFRHHGGHTVSSQKRGPARSHYHDYDEPPEGLWPHD---EGG 3643
Qy 611 PESDFCLKVEAAVLGATGPADSQHSQHG-----GLDQDG-----EARP- 649
Db 3644 PGRH-----TSAXEHRHSDHGRHSGRHAGEEPCGRRAAKPHARDMGREARPH 3691
Qy 650 -----ALDGSALQPLLTHTV 664
Db 3692 PQASPAPAMKQGPQYFSSADYSQSSRAPSAHYHASEKKGSRQAHGTGSALOPKADTQ 3751
Qy 665 KAGSPSDMPRDSGLYDSSVPSSSELSLPLMEGLSLTDQETSLTSVSSSSGLGEEPPAL 724
Db 3752 AQPMQGRQAAAPGQQSQPPSSRQT---PSGTASRQPTQOQQOQQOQQOGLGQAPOQA 3808
Qy 725 PSK 727
Db 3809 PSQ 3811

RESULT 14
T30851
lysosomal trafficking regulator, long splice form - mouse
N;Alternate names: beige protein homolog
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30851
R;Barbosa, M.D.F.S.; Tchernev, V.T.; Kingmore, S.F.
submitted to the EMBL Data Library, September 1996
A;Description: two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.
A;Reference number: Z20903
A;Accession: T30851
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3788 <BAR>
A;Cross-references: UNIPROT:P97412; EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC530
A;Experimental source: strain C57BL/6J
C;Genetics:
A;Gene: Lyst
A;Map position: 1
C;Keywords: alternative splicing

Query Match 2.7%; Score 107; DB 2; Length 3788;
Best Local Similarity 19.5%; Pred. No. 44;
Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;
Qy 20 GSQLAAGSGRARGADTCGRMKAAARPRLCVANEGVGVPASRNSGLYNITPKYDNCCT 79
Db 651 GETLQGLCGAGPCGLPSPSYR-----QGILP-----SSSEDFLWKWDALAE 695
Qy 80 YLNPVGKHVIADAQNIITISOVACH--DQVAVILWSPGALGIEFLKGRFVILEELKSEG- 136
Db 696 YQNFIFOE--DRLHTQIASHCNLIQKGNVIVQ-----KLYNIFNPVLQGV 743
Qy 137 ---RQCQILKDPKQLNSFKRTGMSQPLNKKFT-DYFVKVP-----FP 181
Db 744 ELVHCQQLSI-----TSAQTHMSSQLKQYLPQEVLIQIYKLTPLILLKSRVIRDLFL 795
Qy 182 SIKN-----ESNY-----HPP-FRTACDLLLOPNLACKPFWKPRNLNISOHGSDMQ 229
Db 796 SCNGVNHIELNYLDGIRSHLSKAFETLIVSLGQQKRAAVPGV---DGLDIOQLSSLS 852
Qy 230 VSPDHAPHNFGFRFFLYHLKHEGPPKRTCKQBTETTSCLLQNVSPGDYIIELVDD 289
Db 853 V-----GPSLHK-----QQASTDPCSRLK-----FYASLRDT 880
Qy 290 TMTTRKVNHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTVWCKRKKQOENIYSHLDE 349
Db 881 DPKKRKTVHQ-----DAHINTINLFCVAF-----LCVSKAEDSDRESAN- 920
Qy 350 ESSSSTY--TAALPRRLRPKPVFLCYSSKDGQNHVV-----OCFAYFLQDFCGCEV 403
Db 921 ESEDTSGYDSTASEPLSHMLPRLSL-----ENVVLPSPCELIH----- 958
Qy 404 ALDLWEDFSLCREGRENW--IQTHESQFI-----IVVCSKGMKYFVDKKNYKKGGRG 457
Db 959 AADTW---SMCK-----WYMLNSVFOQFHRLGQFQVCHB-LIFMIQKLFHRTEDQG 1009
Qy 458 SGKELF-----LVAVSAIAEKLRQAKQSSAALSKEFIAYVFDYSCEDGVPGLD----- 507
Db 1010 RQGEMSVNKGQGLMRIIOPEMILKEDYSSSTAPEPGFLKKSADRVSELESQHMLPTSAB 1069
Qy 508 --LSTK-----YRLMDNLPLQCSH-----LHSRDHGLQEPGQHTROG 542
Db 1070 QILATKSPGAKTPMNOESETCLQSIIRLESLLAICLHSARASQKMELELPSQ----- 1124
Qy 543 SRNRYFRSKSGSLVACNMHQFIDEP-----DWFEKQFVFPFPPPLRYREP 591
Db 1125 -----SLSENILCELDHLSQSKVAETELAKPLFDALLKVALGNHSAIDLPGDT 1174
Qy 592 VLEKFDGLVLDNMCKPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646
Db 1175 VTEKSHPS---EVLVSQPGDFSEAEEDSQCSLKLGLGEEGYEADSESNPEDGETQDDGV 1231
Qy 647 ARPALDG--SAALQOP--LLHTVKAG 667
Db 1232 ELPEAEGFSGSVIPNNLLESLTHG 1255

RESULT 13
T42730
Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42730

Query Match 2.7%; Score 107; DB 2; Length 3788;
Best Local Similarity 19.5%; Pred. No. 44;
Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;
Qy 20 GSQLAAGSGRARGADTCGRMKAAARPRLCVANEGVGVPASRNSGLYNITPKYDNCCT 79
Db 651 GETLQGLCGAGPCGLPSPSYR-----QGILP-----SSSEDFLWKWDALAE 695
Qy 80 YLNPVGKHVIADAQNIITISOVACH--DQVAVILWSPGALGIEFLKGRFVILEELKSEG- 136
Db 696 YQNFIFOE--DRLHTQIASHCNLIQKGNVIVQ-----KLYNIFNPVLQGV 743
Qy 137 ---RQCQILKDPKQLNSFKRTGMSQPLNKKFT-DYFVKVP-----FP 181
Db 744 ELVHCQQLSI-----TSAQTHMSSQLKQYLPQEVLIQIYKLTPLILLKSRVIRDLFL 795
Qy 182 SIKN-----ESNY-----HPP-FRTACDLLLOPNLACKPFWKPRNLNISOHGSDMQ 229
Db 796 SCNGVNHIELNYLDGIRSHLSKAFETLIVSLGQQKRAAVPGV---DGLDIOQLSSLS 852
Qy 230 VSPDHAPHNFGFRFFLYHLKHEGPPKRTCKQBTETTSCLLQNVSPGDYIIELVDD 289
Db 853 V-----GPSLHK-----QQASTDPCSRLK-----FYASLRDT 880
Qy 290 TMTTRKVNHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTVWCKRKKQOENIYSHLDE 349
Db 881 DPKKRKTVHQ-----DAHINTINLFCVAF-----LCVSKAEDSDRESAN- 920
Qy 350 ESSSSTY--TAALPRRLRPKPVFLCYSSKDGQNHVV-----OCFAYFLQDFCGCEV 403
Db 921 ESEDTSGYDSTASEPLSHMLPRLSL-----ENVVLPSPCELIH----- 958
Qy 404 ALDLWEDFSLCREGRENW--IQTHESQFI-----IVVCSKGMKYFVDKKNYKKGGRG 457
Db 959 AADTW---SMCK-----WYMLNSVFOQFHRLGQFQVCHB-LIFMIQKLFHRTEDQG 1009
Qy 458 SGKELF-----LVAVSAIAEKLRQAKQSSAALSKEFIAYVFDYSCEDGVPGLD----- 507
Db 1010 RQGEMSVNKGQGLMRIIOPEMILKEDYSSSTAPEPGFLKKSADRVSELESQHMLPTSAB 1069
Qy 508 --LSTK-----YRLMDNLPLQCSH-----LHSRDHGLQEPGQHTROG 542
Db 1070 QILATKSPGAKTPMNOESETCLQSIIRLESLLAICLHSARASQKMELELPSQ----- 1124
Qy 543 SRNRYFRSKSGSLVACNMHQFIDEP-----DWFEKQFVFPFPPPLRYREP 591
Db 1125 -----SLSENILCELDHLSQSKVAETELAKPLFDALLKVALGNHSAIDLPGDT 1174
Qy 592 VLEKFDGLVLDNMCKPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646
Db 1175 VTEKSHPS---EVLVSQPGDFSEAEEDSQCSLKLGLGEEGYEADSESNPEDGETQDDGV 1231
Qy 647 ARPALDG--SAALQOP--LLHTVKAG 667
Db 1232 ELPEAEGFSGSVIPNNLLESLTHG 1255

RESULT 13
T42730
Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42730

Query Match 2.7%; Score 107; DB 2; Length 3788;
Best Local Similarity 19.5%; Pred. No. 44;
Matches 156; Conservative 104; Mismatches 288; Indels 254; Gaps 44;
Qy 20 GSQLAAGSGRARGADTCGRMKAAARPRLCVANEGVGVPASRNSGLYNITPKYDNCCT 79
Db 651 GETLQGLCGAGPCGLPSPSYR-----QGILP-----SSSEDFLWKWDALAE 695
Qy 80 YLNPVGKHVIADAQNIITISOVACH--DQVAVILWSPGALGIEFLKGRFVILEELKSEG- 136
Db 696 YQNFIFOE--DRLHTQIASHCNLIQKGNVIVQ-----KLYNIFNPVLQGV 743
Qy 137 ---RQCQILKDPKQLNSFKRTGMSQPLNKKFT-DYFVKVP-----FP 181
Db 744 ELVHCQQLSI-----TSAQTHMSSQLKQYLPQEVLIQIYKLTPLILLKSRVIRDLFL 795
Qy 182 SIKN-----ESNY-----HPP-FRTACDLLLOPNLACKPFWKPRNLNISOHGSDMQ 229
Db 796 SCNGVNHIELNYLDGIRSHLSKAFETLIVSLGQQKRAAVPGV---DGLDIOQLSSLS 852
Qy 230 VSPDHAPHNFGFRFFLYHLKHEGPPKRTCKQBTETTSCLLQNVSPGDYIIELVDD 289
Db 853 V-----GPSLHK-----QQASTDPCSRLK-----FYASLRDT 880
Qy 290 TMTTRKVNHYALKPVHSPWAGPIRAVAITVPLVVISAPATLFTVWCKRKKQOENIYSHLDE 349
Db 881 DPKKRKTVHQ-----DAHINTINLFCVAF-----LCVSKAEDSDRESAN- 920
Qy 350 ESSSSTY--TAALPRRLRPKPVFLCYSSKDGQNHVV-----OCFAYFLQDFCGCEV 403
Db 921 ESEDTSGYDSTASEPLSHMLPRLSL-----ENVVLPSPCELIH----- 958
Qy 404 ALDLWEDFSLCREGRENW--IQTHESQFI-----IVVCSKGMKYFVDKKNYKKGGRG 457
Db 959 AADTW---SMCK-----WYMLNSVFOQFHRLGQFQVCHB-LIFMIQKLFHRTEDQG 1009
Qy 458 SGKELF-----LVAVSAIAEKLRQAKQSSAALSKEFIAYVFDYSCEDGVPGLD----- 507
Db 1010 RQGEMSVNKGQGLMRIIOPEMILKEDYSSSTAPEPGFLKKSADRVSELESQHMLPTSAB 1069
Qy 508 --LSTK-----YRLMDNLPLQCSH-----LHSRDHGLQEPGQHTROG 542
Db 1070 QILATKSPGAKTPMNOESETCLQSIIRLESLLAICLHSARASQKMELELPSQ----- 1124
Qy 543 SRNRYFRSKSGSLVACNMHQFIDEP-----DWFEKQFVFPFPPPLRYREP 591
Db 1125 -----SLSENILCELDHLSQSKVAETELAKPLFDALLKVALGNHSAIDLPGDT 1174
Qy 592 VLEKFDGLVLDNMCKPESDFCLKVEAAVLGATG-----PADSQHESQHGGLDQDGE 646
Db 1175 VTEKSHPS---EVLVSQPGDFSEAEEDSQCSLKLGLGEEGYEADSESNPEDGETQDDGV 1231
Qy 647 ARPALDG--SAALQOP--LLHTVKAG 667
Db 1232 ELPEAEGFSGSVIPNNLLESLTHG 1255

Qy 20 GSQLAAGGGRGADTCGRMKAAPRLCVANEGVGPASRNSGLYNITFKYDNCCTT 79
Db 651 GETLOGLCGAGPTSLGPSYRF-----QGILP-----SSGEDLLKWDALAE 695
Qy 80 YLNPVGKHVADANITISQVACH--DQAVATILWSPGALGIEFLKGRFVILEELKSEG- 136
Db 696 YQSFFVQF--DRLHNIQIANHICNLLQKGNVVQW-----KLYNIFNVLQRGV 743
Qy 137 ---RQCQOLILKDPKQLNSSKFRIMESQPLNMKFET-DYFVKVVP-----FP 181
Db 744 ELVHHCQQLSIPS-----AQTHMCSQLKQYLPOEVLQIYLYLTKPLVLLKSRVIRDLFL 795
Qy 182 SIKN-----EGNY-----HPP-FPRTRACDLLQPDNLACKPFWKPRNLNISQHSQDMQ 229
Db 796 SCNGVNHIEILNYLDIRSHSLKAFETLIVSLGQQKDAVLDV---DGLDIOBELSLIS 852
Qy 230 VSFDPHAFNFGFRFFYLHYKLKHEGPFKPKCKOEQTITETTSCLLQNVSPGDYIIELVDD 289
Db 853 V-----GPSLHK-----QOASSDSPCSLRK-----FYASLREP 880
Qy 290 TINTKVMHYALKPVHSPWAGPIRAVAITVPLVISAPATLFTVMCKKKQENIYSHLDE 349
Db 881 DPKRKRTI--QDVH-----INTINLFLCVAF-----LCVSKHEADS-----DR 916
Qy 350 ESSESSTYTAALPRRLRPRKPVFLCYSSKDGQNHMVV---OCFAFYFLQDFCGCEVAL 405
Db 917 ESANESDTSYDPPSPPELHMLPCLSLD-----VLPSPECLHH-----AA 960
Qy 406 DLWEDFSLCREGREW--IOKIHESQFI-----IWCCKGMKYFVDKKNYKHGGGRSG 459
Db 961 DIW---SMCR-----WIYMLNSVFQKQPHRLGGFQVCHE-LIFMIIOKLPFSHTEDQRR 1011
Qy 460 KGELF-----LVAVSAEAKLROAKQSSAALSKEFTAVFYDYSCGDVPGIL--DLSTK 511
Db 1012 QGEMSRNENQELIRIS-----YPELTKGDVSSATAPDLGFL 1048
Qy 512 YRLMDN-----LPOLCSHLHSRDHGLQEPGQHTQGRSRRNVFERSKGRSLYVAICN 562
Db 1049 RKSADSVRGFSQVPLPVSABQIVATE---SVPGE-----RKAFMSQOSETSLQIRL 1098
Qy 563 MHQFIDEPDFEKFQVFPFHPPLRYRBPVLEKFDGSLVLMNDVMCK-----608
Db 1099 LESLLD-----ICLHSARACQKQMLELSPQGLSVENILCELREHLSQSKVAETE 1148
Qy 609 -PGESPDLKVEAAVLGA-TGPADS-----QHESQHGGLDQDGEARPALDGSAAALQPLH 662
Db 1149 LAKPLFDALLRVLGNHSAIDLPGDAVTEKSHPSSEELLSQPGDFSEAEADSQCCSLKL 1208
Qy 663 TVKAGSPSDM---PRDSGIYDSSVPSPSLPLMEGLSTQDTETSSLTESVSSSSGLGE- 718
Db 1209 GEEGYEADSENEDVUTQDGV---ELN-PEAEGFS-GSIVSNLLENLTH-----GEI 1259
Qy 719 --EPPALPSKLLSGSCADL 738
Db 1260 IYPEICMLGLNLSASKALDV 1281

RESULT 15

D86477
protein F1504.27 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86477
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86477
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-638 <STO>
A:Cross-references: UNIPROT:Q9LQF8; GB:AE005172; NID:g8778345; PIDN:AAF79353.1; GSPDB:GM
C:Genetics:
A:Gene: F1504.27
A:Map position: 1

Query Match 2.7%; Score 106.5; DB 2; Length 638;
Best Local Similarity 19.4%; Pred. No. 3.4;
Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

Qy 94 NIITISQACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRCQOOLILKDPKQLNSS 153
Db 275 DIKYGQYSCHLODFCYVYVHS-----KCATHENYMDGKELEWEIETEDDISP 322
Qy 154 FKRTGMSQFFLNMKPFETDYFVKVVPFP---SIKNESNYHPFFRTRACDLLQPDNLAC 210
Db 323 FRNLG-----DGFIKHFCHKHRLKLNHGDGARDTEKQCRAC---IYP--IVS 364
Qy 211 KPFWKPRNLNISQHG--SDMQVSFDRHAPNFGFRFFYLHYKLKHEGP--FKRKTCKOEQT 266
Db 365 HQFVHCCKKNYSLHEVCAGLSRKLDAHNN-----HTLILSPSPGKCCSACSREST 416
Qy 267 TETTSCLLQNVSPGDYIIELVDDTNTYKVMHYALKPVHSPWAGPIRAVAITVPLVISA 326
Db 417 GFSYIC--SNKGCQDFLDV-----RCISVLEYFIHRSHEH-----PIFISTS 457
Qy 327 FATLFTVMCKKQOENIYSHLDEESSE--SSTYTAALPRE---RLRPRPKVFLCYSGSKOG 381
Db 458 YNSKDEILCKVKRCRCLGAHLQCLCEFTWCYSCAIPDEIHYKFKDKHPLTLSCGESAD- 516
Qy 382 QNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCRGEGREWVIQKIHESQFIIVVCSKGMK 441
Db 517 ---NTYWCEV-----CEKQDPKEWFTCNK-----CCITIH-----LHCIFGSS 553
Qy 442 YFVDKKNYKHGGGRSGKGEFLVAVSAEAKLROAKQSSAALSKEFTAVFYDYSCGD 501
Db 554 VFM-----KPG-----SIFRDYDGKVQ 570
Qy 502 VPGILDLSLTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTQGRSRRN--YFRSKSGRSLY-V 558
Db 571 V-----FRNSNTRQLCYMCHNRCTGL-----IPFEGYRRNATYYNHSNRSTHRM 616
Qy 559 AICNM 563
Db 617 IFCSL 621

Search completed: August 9, 2005, 11:49:54
Job time : 35.2019 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:36:31 ; Search time 118.76 Seconds
(without alignments)
3246.847 Million cell updates/sec

Title: US-10-717-282-2
Perfect score: 4013
Sequence: 1 MAPWLQCSVFTVNACING.....CKADLGCRSYDELHVAAPL 753

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 3319 | 97.7 | 739 | 2 Q8NFS0 | Q8nfs0 homo sapien |
| 2 | 3315 | 97.6 | 739 | 2 Q8NFM7 | Q8nfm7 homo sapien |
| 3 | 3708 | 92.4 | 707 | 2 Q6RVE4 | Q6rvf4 homo sapien |
| 4 | 3703 | 92.3 | 728 | 2 Q6UW15 | Q6uw15 homo sapien |
| 5 | 3401.5 | 84.8 | 738 | 2 Q8JZL1 | Q8jz11 mus musculus |
| 6 | 3170 | 79.0 | 595 | 2 Q8N113 | Q8n113 homo sapien |
| 7 | 3005 | 74.9 | 564 | 2 Q9UFA0 | Q9ufa0 homo sapien |
| 8 | 2892 | 72.1 | 741 | 2 Q7T2L7 | Q7t2l7 gallus gall |
| 9 | 2834 | 70.6 | 697 | 2 Q8AV76 | Q8av76 gallus gall |
| 10 | 2675.5 | 66.7 | 594 | 2 Q8K447 | Q8k447 mus musculus |
| 11 | 2616.5 | 65.2 | 582 | 2 Q8R5J8 | Q8r5j8 mus musculus |
| 12 | 1961 | 48.9 | 745 | 2 Q8QHJ9 | Q8qhj9 brachydanio |
| 13 | 1952 | 48.6 | 745 | 2 Q8QHJ6 | Q8qhj6 brachydanio |
| 14 | 538 | 13.4 | 109 | 2 Q8HXE8 | Q8hxe8 macaca fasc |
| 15 | 310 | 7.7 | 866 | 1 I17R_HUMAN | Q95f46 homo sapien |
| 16 | 306 | 7.6 | 864 | 1 I17R_MOUSE | Q60943 mus musculus |
| 17 | 205 | 5.1 | 769 | 2 Q69HQ3 | Q69hq3 ciona intes |
| 18 | 170.5 | 4.2 | 846 | 2 Q9NA64 | Q9na64 caenorhabdi |
| 19 | 135.5 | 3.4 | 502 | 1 I17S_HUMAN | Q9nmr6 homo sapien |
| 20 | 126.5 | 3.2 | 718 | 1 YS02_CAEEL | Q10128 caenorhabdi |
| 21 | 121 | 3.0 | 993 | 2 Q7PWU5 | Q7pwu5 anopheles g |
| 22 | 117.5 | 2.9 | 562 | 2 Q99755 | Q99755 homo sapien |
| 23 | 117 | 2.9 | 757 | 2 O13399 | O13399 ustilago ma |
| 24 | 117 | 2.9 | 917 | 2 O81789 | O81789 arabidopsis |
| 25 | 117 | 2.9 | 2946 | 2 Q64634 | Q64634 arabidopsis |
| 26 | 116.5 | 2.9 | 637 | 2 Q6AZ51 | Q6az51 rattus norv |
| 27 | 116.5 | 2.9 | 901 | 2 Q9KE04 | Q9ke04 bacillus ha |
| 28 | 116 | 2.9 | 4736 | 2 Q7YT99 | Q7ytc99 mytilus gal |
| 29 | 115.5 | 2.9 | 938 | 2 Q60669 | Q60669 mus musculus |
| 30 | 115 | 2.9 | 859 | 1 MR1P_HUMAN | Q8ntw9 homo sapien |
| 31 | 115 | 2.9 | 998 | 1 EPB3_HUMAN | P54753 homo sapien |

ALIGNMENTS

RESULT 1

| ID | Q8NFS0 | PRELIMINARY; | PRT; | 739 AA. |
|----|---|--------------|------|---------|
| AC | Q8NFS0; | | | |
| DT | 01-OCT-2002 (Tremblrel. 22, Created) | | | |
| DT | 01-OCT-2002 (Tremblrel. 22, Last sequence update) | | | |
| DT | 01-MAR-2004 (Tremblrel. 26, Last annotation update) | | | |
| DE | IL-17RD. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Gilbert J.M., Gorman D.M.; | | | |
| RL | Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AF458067; AAM77571.1; -- | | | |
| DR | GO; GO:0016020; C:membrane; IEA. | | | |
| DR | GO; GO:0004888; F:transmembrane receptor activity; IEA. | | | |
| DR | InterPro; IPR000157; TIR. | | | |
| SQ | SEQUENCE 739 AA; 82440 MW; 1670803DD0CDOF17 CRC64; | | | |

| | | | | |
|-----------------------|--------|----------------------------|--|---------------|
| Query Match | 97.7%; | Score 3919; | DB 2; | Length 739; |
| Best Local Similarity | 98.0%; | Pred. No. 2.2e-290; | | |
| Matches | 738; | Conservative | 0; | Mismatches 1; |
| | | | | Indels 14; |
| | | | | Gaps 1; |
| QY | 1 | MAPWLQCSVFTVNACINGSQLA | VAAGSGRGARGADTCGWRMKAARPRLCVANEGVGP | 60 |
| | | | | |
| Db | 1 | MAPWLQCSVFTVNACINGSQLA | VAAGSGRGARGADTCGWRMKAARPRLCVANEGVGP | 46 |
| | | | | |
| QY | 61 | ASRNSGLYNIITFKYDNCITTYLNPV | GKHVIADAQNTITISQYACHDQVAVTILWSPGALGIE | 120 |
| | | | | |
| Db | 47 | ASRNSGLYNIITFKYDNCITTYLNPV | GKHVIADAQNTITISQYACHDQVAVTILWSPGALGIE | 106 |
| | | | | |
| QY | 121 | FLKGRVILEELKSGRGCOQILKDP | QKLNSFKRTGMSQPFLLMKFETDYFKVVPVF | 180 |
| | | | | |
| Db | 107 | FLKGRVILEELKSGRGCOQILKDP | QKLNSFKRTGMSQPFLLMKFETDYFKVVPVF | 166 |
| | | | | |
| QY | 181 | PSIKNESNYHPPFFTRACDILLQ | PDNLACPFWRPNLINSOHGSDMQVSDHAPHNFG | 240 |
| | | | | |
| Db | 167 | PSIKNESNYHPPFFTRACDILLQ | PDNLACPFWRPNLINSOHGSDMQVSDHAPHNFG | 226 |
| | | | | |
| QY | 241 | FRFFVLYHLKXHEGPFKRTCKEQ | TETTSCLLNQVSPGDYIIELVDDTNTTRKVMHYA | 300 |
| | | | | |
| Db | 227 | FRFFVLYHLKXHEGPFKRTCKEQ | TETTSCLLNQVSPGDYIIELVDDTNTTRKVMHYA | 286 |
| | | | | |
| QY | 301 | LKPVHSPWAGPIRAVAITVPLV | VISAFATLFTVMCRKQEQNIYSHLDESESESYTAA | 360 |
| | | | | |
| Db | 287 | LKPVHSPWAGPIRAVAITVPLV | VISAFATLFTVMCRKQEQNIYSHLDESESESYTAA | 346 |
| | | | | |
| QY | 361 | LPRELRPRPKVFLCYSSKDGQ | GNHMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE | 420 |
| | | | | |
| Db | 347 | LPRELRPRPKVFLCYSSKDGQ | GNHMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE | 406 |
| | | | | |

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QY 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGELFLVAVSAIAEKLRQAKQ 480
DB 407 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGELFLVAVSAIAEKLRQAKQ 466
QY 481 SSSAALSXFIAYFDYSCGDPVPGILDSTKYRLMDNLPQLCSHLHSDHGLQBPQGQHTR 540
DB 467 SSSAALSXFIAYFDYSCGDPVPGILDSTKYRLMDNLPQLCSHLHSDHGLQBPQGQHTR 526
QY 541 QGSRNRYFRSKGSLYVAICNMHOFIDEBPDWFEKQFVPPHPPPLRYRBPVLEKFDPSGL 600
DB 527 QGSRNRYFRSKGSLYVAICNMHOFIDEBPDWFEKQFVPPHPPPLRYRBPVLEKFDPSGL 586
QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHSHQGGDQDGEARPALDGSAAQLQPL 660
DB 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHSHQGGDQDGEARPALDGSAAQLQPL 646
QY 661 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEEE 720
DB 647 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEEE 706
QY 721 PPALPSKLLSSGCKADIGCRSYTDELHVAAPL 753
DB 707 PPALPSKLLSSGCKADIGCRSYTDELHVAAPL 739

RESULT 2
QBNFM7 PRELIMINARY; PRT; 739 AA.
AC Q8NFM7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein long form.
GN Name=IL17RLM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "hsf1 inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Xiong S.Q., Huang G.R., Zhao O.H., Chen P.L., Rong Z.L., Ye X.Y.,
RA Chen Y., Liu L., Fu X.X., Chang Z.J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF494208; AAM74077.1; -.
DR Genew; HGNC:17616; IL17RD.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Receptor.
SQ SEQUENCE 739 AA; 82441 MW; BCDA2A95261B0277 CRC64;

Query Match 97.6%; Score 3915; DB 2; Length 739;
Best Local Similarity 97.9%; Pred. No. 4.5e-290;
Matches 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

QY 1 MAPWLQCSVFTVNAACNGSOLAAGGSGRARGADTCGWRMKAARPRCLCVANEGVGP 60
DB 1 MAPWLQCSVFTVNAACNGSOLAAGGSGRARGADTCGWR-----GVGP 46
QY 61 ASRNSGLNITFKYDNCNTYLNPKVKHVIADAQNITISQYACHDOVAVTILWSPCALGIE 120
DB 47 ASRNSGLNITFKYDNCNTYLNPKVKHVIADAQNITISQYACHDOVAVTILWSPCALGIE 106
QY 121 FLKGFVRVLEELKSGRQCQQLIKDPKQNSFKRTGMESQPLNMFETDYYFKVVPVF 180
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DB 107 FLKGFVRVLEELKSGRQCQQLIKDPKQNSFKRTGMESQPLNMFETDYYFKVVPVF 166
QY 181 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNLNISOHGSMDQVSEFDHAPNFG 240
DB 167 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNLNISOHGSMDQVSEFDHAPNFG 226
QY 241 FRPFLYHLKHGEPFKRKCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
DB 227 FRPFLYHLKHGEPFKRKCKOBTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
QY 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVWCRKKQENIYSHLDESSSESTYTAA 360
DB 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVWCRKKQENIYSHLDESSSESTYTAA 346
QY 361 LPRERLPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
DB 347 LPRERLPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406
QY 421 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGELFLVAVSAIAEKLRQAKQ 480
DB 407 WVIQIHESQFIIVVCSKGMKYFVDKKNYKHGGRSGKGELFLVAVSAIAEKLRQAKQ 466
QY 481 SSSAALSXFIAYFDYSCGDPVPGILDSTKYRLMDNLPQLCSHLHSDHGLQBPQGQHTR 540
DB 467 SSSAALSXFIAYFDYSCGDPVPGILDSTKYRLMDNLPQLCSHLHSDHGLQBPQGQHTR 526
QY 541 QGSRNRYFRSKGSLYVAICNMHOFIDEBPDWFEKQFVPPHPPPLRYRBPVLEKFDPSGL 600
DB 527 QGSRNRYFRSKGSLYVAICNMHOFIDEBPDWFEKQFVPPHPPPLRYRBPVLEKFDPSGL 586
QY 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHSHQGGDQDGEARPALDGSAAQLQPL 660
DB 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHSHQGGDQDGEARPALDGSAAQLQPL 646
QY 661 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEEE 720
DB 647 LHTKAGSPSDMPRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLGEEE 706
QY 721 PPALPSKLLSSGCKADIGCRSYTDELHVAAPL 753
DB 707 PPALPSKLLSSGCKADIGCRSYTDELHVAAPL 739

RESULT 3
Q6RVF4 PRELIMINARY; PRT; 707 AA.
AC Q6RVF4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SEF splice variant b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUES=Testes;
RX PubMed=14742870; DOI=10.1073/pnas.0307952100;
RA Preger E., Ziv I., Shabtay A., Sher I., Tsang M., Dawid I.B.,
RA Altuvia Y., Ron D.;
RT "Alternative splicing generates an isoform of the human Sef gene with
RT altered subcellular localization and specificity.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:1229-1234(2004).
DR EMBL; AY489047; AAS15051.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 707 AA; 79493 MW; 7D3BE21EE038F17E CRC64;

Query Match 92.4%; Score 3708; DB 2; Length 707;
Best Local Similarity 99.7%; Pred. No. 2.8e-274;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

QY 56 EGVGPASRNSGLYNTFKYDNCTTYLNPVGVKHVIADQNITISQYACHDQVAVTILWSPG 115
DB :|||||
10 QGVGPASRNSGLYNTFKYDNCTTYLNPVGVKHVIADQNITISQYACHDQVAVTILWSPG 69
QY 116 ALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSFKRTGMESQPFLLNMKFTDYFV 175
DB :|||||
70 ALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSFKRTGMESQPFLLNMKFTDYFV 129
QY 176 KVPFPPIKSNYHPFFRTRACDLLOPDLNACKPFWKPRNLNISOHSDMOVSFDHA 235
DB :|||||
130 KVPFPPIKSNYHPFFRTRACDLLOPDLNACKPFWKPRNLNISOHSDMOVSFDHA 189
QY 236 PHNFGFFFYLYKHEGPPKRTCKQEQTTETSCILQNVSPGDYIIEILDVDTNTRK 295
DB :|||||
190 PHNFGFFFYLYKHEGPPKRTCKQEQTTETSCILQNVSPGDYIIEILDVDTNTRK 249
QY 296 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQOENIYSHLDESS 355
DB :|||||
250 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKKQOENIYSHLDESS 309
QY 356 TYTAALPRERLRPRPKVPLCYSSKXGQNMNVQCFAYFLQDFCGCEVALDLWEDFSLCR 415
DB :|||||
310 TYTAALPRERLRPRPKVPLCYSSKXGQNMNVQCFAYFLQDFCGCEVALDLWEDFSLCR 369
QY 416 EGQREWIQTHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKL 475
DB :|||||
370 EGQREWIQTHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKL 429
QY 476 RQAKQSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKL 535
DB :|||||
430 RQAKQSSAALSXFIIVVCSKGMKYFVDKKNYKHGGGSGKGLFLVAVSAIAEKL 489
QY 536 QOHTQSGRRNYFRSKSGRSYLYVAINCNHQFIIDEEPWFEXQFVFPFPPPLRYREPVLK 595
DB :|||||
490 QOHTQSGRRNYFRSKSGRSYLYVAINCNHQFIIDEEPWFEXQFVFPFPPPLRYREPVLK 549
QY 596 FDSGLVNDVCKPESDCLKVEAAVLGATGPDADSOHSGHGLDQDGEARPDGSA 655
DB :|||||
550 FDSGLVNDVCKPESDCLKVEAAVLGATGPDADSOHSGHGLDQDGEARPDGSA 609
QY 656 ALQPLLLHTVKAGSPDMPDRDGSIGYDSSVSPSELSLPLMEGLSTDQTTSSITSSVSSG 715
DB :|||||
610 ALQPLLLHTVKAGSPDMPDRDGSIGYDSSVSPSELSLPLMEGLSTDQTTSSITSSVSSG 669
QY 716 LGEEPPALPKLLSSGCKADLCGRSYTDELHVAAPL 753
DB :|||||
670 LGEEPPALPKLLSSGCKADLCGRSYTDELHVAAPL 707

RESULT 4

Q6UW15 PRELIMINARY; PRT; 728 AA.
ID Q6UW15
AC Q6UW15
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE IL17Rhom.
GN ORFNames=UNQ6115;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yaneura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358774; AA089134.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 728 AA; 81310 MW; 4AD9D3F6B1C78C26 CRC64;

Query Match 92.3%; Score 3703; DB 2; Length 728;
Best Local Similarity 96.7%; Pred. No. 6.9e-274;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

QY 42 RMKAAARPRLCVANE-GVGPASRNSGLYNTFKYDNCTTYLNPVGVKHVIADQNITISQY 100
DB :|||||
3 RASAGVPAALFVSGEQGVGPASRNSGLYNTFKYDNCTTYLNPVGVKHVIADQNITISQY 62
QY 101 ACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSFKRTGM 160
DB :|||||
63 ACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSFKRTGM 122
QY 161 SQPPLNMKFTDYFVVPVPPPSIKNESNYHPFFRTRACDLLOPDLNACKPFWKPRNLN 220
DB :|||||
123 SQPPLNMKFTDYFVVPVPPPSIKNESNYHPFFRTRACDLLOPDLNACKPFWKPRNLN 182
QY 221 ISQ-----HGSDMOVSFDHAPHNFGFRFFLYKHEGPFKRKTCQEQTT 267
DB :|||||
183 ISQHSQSDMOVSFDHAPHNFGFRFFLYKHEGPFKRKTCQEQTT 242
QY 268 ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 327
DB :|||||
243 EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 302
QY 328 ATLFVVMCRKQKQENIYSHLDESSSTYTAALPRERLRPRPKVFLCYSKDQGNHNV 387
DB :|||||
303 ATLFVVMCRKQKQENIYSHLDESSSTYTAALPRERLRPRPKVFLCYSKDQGNHNV 362
QY 388 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQTHESQFIIVVCSKGMKYFVDK 447
DB :|||||
363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQTHESQFIIVVCSKGMKYFVDK 422
QY 448 NYKHGGGSGKGLFLVAVSAIAEKLRAQKSSAALSXFIIVVCSKGMKYFVDK 507
DB :|||||
423 NYKHGGGSGKGLFLVAVSAIAEKLRAQKSSAALSXFIIVVCSKGMKYFVDK 482
QY 508 LSTKYRLMDNLPQLCSHLHSRDHGLQBPQOHTQSGRRNYFRSKSGRSYLYVAINCNHQFI 567
DB :|||||
483 LSTKYRLMDNLPQLCSHLHSRDHGLQBPQOHTQSGRRNYFRSKSGRSYLYVAINCNHQFI 542
QY 568 DEEPDWFEXQFVFPFPPPLRYREPVLKFDGSLVNDVCKPESDCLKVEAAVLGAT 627
DB :|||||
543 DEEPDWFEXQFVFPFPPPLRYREPVLKFDGSLVNDVCKPESDCLKVEAAVLGAT 602
QY 628 GPADSQHSQHGLDQDGEARPDGSAALQPLLLHTVKAGSPDMPDRDGSIGYDSSVSPSE 687
DB :|||||
603 GPADSQHSQHGLDQDGEARPDGSAALQPLLLHTVKAGSPDMPDRDGSIGYDSSVSPSE 662
QY 688 LSLPLMEGLSTDQTTSSITSSVSSGGLGEEPPALPKLLSSGCKADLCGRSYTDEL 747
DB :|||||
663 LSLPLMEGLSTDQTTSSITSSVSSGGLGEEPPALPKLLSSGCKADLCGRSYTDEL 722
QY 748 HAVAPL 753
DB :|||||
723 HAVAPL 728

RESULT 5

Q8JZL1
ID Q8JZL1 PRELIMINARY; PRT; 738 AA.
AC Q8JZL1

DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Transmembrane protein (interleukin 17 receptor-like protein long form).
 DE Name=1117rd; Synonyms=1117rlm, Sef;
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21959295; PubMed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
 RA Lin W., Furthauer M., Thiesse B., Thiesse C., Jing N., Ang S.-L.;
 RT "Cloning of the mouse Sef gene and comparative analysis of its
 expression with Fgf8 and Spry2 during embryogenesis.";
 RL Mech. Dev. 113:163-168(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=BALB/c;
 RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
 RA Liu L., Chang Z.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF459444; AAM28441.1; -;
 DR EMBL; AF494210; AAM74079.1; -;
 DR MGD; MGI:2159727; 1117rd.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR InterPro; IPR00157; TIR.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
 KW Receptor; Transmembrane
 SQ SEQUENCE 738 AA; 82347 MW; DSCB66230E3E8226 CRC64;
 Query Match 84.8%; Score 3401.5; DB 2; Length 738;
 Best Local Similarity 85.4%; Pred. No. 7.6e-251;
 Matches 646; Conservative 37; Mismatches 52; Indels 21; Gaps 5;
 QY 1 MAPWLQCSFPTVNAVLGSLQAVAGGSGRARGADTCGRMKAAARPLCVANEGVGP 60
 DB 1 MAPWLQCSFPTVNAVLGSLQAVAGGSGRARGADTCGRW-----GVGP 46
 QY 61 ASRNSGLYNTFFKDYNDCTYLPVNGKVIADAQNTISOVACHDQVAVTILWSPGALGIE 120
 DB 47 ASRNSGLHNTFFRYDNTCTYLPNGKGAIADAQNTISQVACHDQVAVTILWSPGALGIE 106
 QY 121 FLKGFRVILELSEKGRQCQQLILKDPKQLNSSFRRTGMSQPFLNKKFTDYFVKVVPF 180
 DB 107 FLKGFRVILELSEKGRQCQQLILKDPKQLNSSFRRTGMSQPFLNKKFTDYFVKVVPF 166
 QY 181 PSIKNESNYHPPFRTRACDILLOPDNLACKFPFKPKNLNIHQGSDMKQVSDHAPNFG 240
 DB 167 PSIKNESNYHPPFRTRACDILLOPDNLACKFPFKPKNLNIHQGSDMHVSFDHAPNFG 226
 QY 241 PRFVLYHLKHGEPFKRCKTCKQSTTETTSCLQNVSFGDYIILELVDNTTTRKVMHYA 300
 DB 227 PRGFVLYHLKHGEPFKRRTCKQNTTETTSCLQNVSFGDYIILELVDNNTTRKAAQYV 286
 QY 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYAA 360
 DB 287 VKSVQSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSPSTYAAA 346
 QY 361 LPRELRPRPKVFLCYSSKDGQNHMMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
 DB 347 LPRELRPRPKVFLCYSSKDGQNHMMNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406
 QY 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGFELVAVSAIAEKLROAKQ 480
 DB 407 WAIQKIHESQFIIVVCSKGMKYFVDKKNPRHKGSGRGEAQEFELVAVAAIAEKLROAKQ 466
 QY 481 SSSAALSFTAVFYDYSCEGDVFGILDLSTKYRLMDNLPCSLHLSRDHGLQEP-CQHT 539
 DB 467 SSSAALSFTAVFYDYSCEGDVPCSLDLSTKYRLMDHLPCLCAHLS---GEQEVLGQHP 523
 QY 540 RQSGRRNYFRSKSGRSILYVAICNMHQFIDEEPWFKEQFVFPFPPPLRYREPVLKEKDSG 599
 DB 524 GHSRRNYFRSKSGRSILYVAICNMHQFIDEEPWFKEQFIPFPQPPVRYQEPVLKEKDSG 583
 QY 600 LVLDNVMCKPGPESDFCLKVEAAVLGATGPAADSOH--ESQHGGLDQDGEARPALDGSAAAL 657
 DB 584 LVLDNVMCKPGPESDFCLKVEACVGLGAAGPADSVSYLESQHVGLDQDTEAQPSCDSAPAL 643
 QY 658 QPLLHTVTKAGSPDMPRDSGIYDSSVPSSSELSPLMBGLSTDTQETSSLTSSSSSGLG 717
 DB 644 QPLLHAVTKAGSPSEMPRDSGIYDSSVPSSSELSPLMBGLSPDQIETSSLTSSSSSGLG 703
 QY 718 EESPPALPSKLLSSGCKADLGCRSYTDLHVAAPL 753
 DB 704 EEDPPTLPKLLASGVSR-BHGCHSHTDELQALPL 738
 RESULT 6
 Q8N113 PRELIMINARY; PRT; 595 AA.
 AC Q8N113;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Interleukin 17 receptor-like protein short form (Hypothetical protein DKFZp434L0320).
 DE Names=1117RLM; Synonyms=DKFZp434L0320;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
 RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
 RA Liu L., Chang Z.;
 RT "hSef inhibits PC-12 cell differentiation by interfering with Ras-mitogen-activated protein kinase MAPK signaling.";
 RL J. Biol. Chem. 278:50273-50282(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Ottenwaelder B., Obermaier B., Mewes H.W., Gaassenhuber J., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF494211; AAM74080.1; -;
 DR EMBL; AL833913; CAD38769.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR000157; TIR.
 KW Hypothetical protein; Receptor.
 SQ SEQUENCE 595 AA; 66846 MW; 7E6BBB64F73B2112 CRC64;
 Query Match 79.0%; Score 3170; DB 2; Length 595;
 Best Local Similarity 99.8%; Pred. No. 2.7e-233;
 Matches 594; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 159 MESQPLNKKFETDYFVKVVPFPSIKNESNYHPPFRTRACDILLOPDNLACKFPFKPRN 218
 DB 1 MESQPLNKKFETDYFVKVVPFPSIKNESNYHPPFRTRACDILLOPDNLACKFPFKPRN 60

QY 219 LNISHQSDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRTCKQEQTTETTSCLLNQVS 278
 DB 61 LNISHQSDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRTCKQEQTTETTSCLLNQVS 120
 QY 279 PGDYIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 338
 DB 121 PGDYIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180
 QY 339 QQENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKGQNMNVVQCFAYFLQDF 398
 DB 181 QQENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKGQNMNVVQCFAYFLQDF 240
 QY 399 CGCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGS 458
 DB 241 CGCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGS 300
 QY 459 KGKELFLVAVSAIAEKLRAQKSSAALSKEIAYVDFYSCGDVPGIILDLSTKYRLMDNL 518
 DB 301 KGKELFLVAVSAIAEKLRAQKSSAALSKEIAYVDFYSCGDVPGIILDLSTKYRLMDNL 360
 QY 519 POLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNNHQFIDEEPWFKEQF 578
 DB 361 POLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNNHQFIDEEPWFKEQF 420
 QY 579 VPFHPPLRYREPVLKEFDSGLVLDNMVCKPESDFCLKVEAAVLGATGPADSOHESQH 638
 DB 421 VPFHPPLRYREPVLKEFDSGLVLDNMVCKPESDFCLKVEAAVLGATGPADSOHESQH 480
 QY 639 GGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSSELSLPLMEGLST 698
 DB 481 GGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSSELSLPLMEGLST 540
 QY 699 DQETSSLTESVSSSGGLGEEPPALPSKLLSSGCKADLGRSYTDELHAVAPL 753
 DB 541 DQETSSLTESVSSSGGLGEEPPALPSKLLSSGCKADLGRSYTDELHAVAPL 595

RESULT 7

Q9UFA0 PRELIMINARY; PRT; 564 AA.
 AC Q9UFA0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp34N1928 (Fragment).
 GN Name=DKFZp34N1928;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Testis;
 RA Bloeker H., Boeher M., Brandt P., Mewes H.W., Gassenhuber J.,
 RA Wiemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133097; CAB61408.1; -;
 DR PIR; T42695; T42695.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR000157; TIR.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 564 AA; 63134 MW; 6B3AASBD4523E88C CRC64;

Query Match 74.9%; Score 3005; DB 2; Length 564;
 Best Local Similarity 99.8%; Pred. No. 1e-220;
 Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 190 HPFFRTRACDLLLPDNLACKPFWKPRNLNLSQHGSDMQVSFDHAPHNFGFRFFYLHYK 249
 DB 1 HPFFRTRACDLLLPDNLACKPFWKPRNLNLSQHGSDMQVSFDHAPHNFGFRFFYLHYK 60

QY 250 LKHEGPFKRTCKQEQTTETTSCLLNQVSPGDYIELVDDTNTTRKVMHYALKPVHSPWA 309
 DB 61 LKHEGPFKRTCKQEQTTETTSCLLNQVSPGDYIELVDDTNTTRKVMHYALKPVHSPWA 120
 QY 310 GPTRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSESTYTAALPRERLRPR 369
 DB 121 GPTRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSESTYTAALPRERLRPR 180
 QY 370 PKVFLCYSSKGQNMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQIHES 429
 DB 181 PKVFLCYSSKGQNMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQIHES 240
 QY 430 QFIIVVCSKGMKYFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSAALSKEF 489
 DB 241 QFIIVVCSKGMKYFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRAQKSSAALSKEF 300
 QY 490 IAVYDFYSCGDVPGIILDLSTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTROGSRNRYFR 549
 DB 301 IAVYDFYSCGDVPGIILDLSTKYRLMDNLPLQCSHLHSRDHGLQEPGQHTROGSRNRYFR 360
 QY 550 SKGRSLYVAICNNHQFIDEEPWFKEQFVFPFHPPLRYREPVLKEFDSGLVLDNMVCKP 609
 DB 361 SKGRSLYVAICNNHQFIDEEPWFKEQFVFPFHPPLRYREPVLKEFDSGLVLDNMVCKP 420
 QY 610 GPESDFCLKVEAAVLGATGPADSOHESQHGLDQDGEARPALDGSAAALQPLLHTVKAGSP 669
 DB 421 GPESDFCLKVEAAVLGATGPADSOHESQHGLDQDGEARPALDGSAAALQPLLHTVKAGSP 480
 QY 670 SDMPRDSGIYDSSVPSSSELSLPLMEGLSTQETSSLTESVSSSGGLGEEPPALPSKLL 729
 DB 481 SDMPRDSGIYDSSVPSSSELSLPLMEGLSTQETSSLTESVSSSGGLGEEPPALPSKLL 540
 QY 730 SSGCKADLGRSYTDELHAVAPL 753
 DB 541 SSGCKADLGRSYTDELHAVAPL 564

RESULT 8

Q7T2L7 PRELIMINARY; PRT; 741 AA.
 AC Q7T2L7
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FGF signaling antagonist SEF.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22660508; PubMed=12766772; DOI=10.1038/ncb989;
 RA Kawakami Y., Rodriguez-Leon J., Roth C.M., Buscher D., Itoh T.,
 RA Rava A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
 RA Schwarz M.-F., Asahara H., Izpisua Belmonte J.C.;
 RT "MKP3 mediates the cellular response to FGF8 signalling in the
 RT vertebrate limb";
 RL Nat. Cell Biol. 5:513-519(2003).
 DR EMBL; AY278204; AAP70001.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR000157; TIR.
 SQ SEQUENCE 741 AA; 83553 MW; 64B8B88241AC60CF CRC64;

Query Match 72.1%; Score 2892; DB 2; Length 741;
 Best Local Similarity 72.4%; Pred. No. 6.4e-212;
 Matches 548; Conservative 79; Mismatches 110; Indels 20; Gaps 6;

QY 1 MAPLQLCSVFVTNACLNGSQLAVAGGSGRANG--ADTCGWRMKAARPRCLCVANEGV 58
 DB 1 MAPRELGAFLALLAFCGGRLFAAGGPGGRGAADACGGR-----GL 46

Qy 59 GPASRNSGLNITFKYDNCTTILNVPVGHVIADQNITISQYACHQDVAVTILMSPGALG 118
Db : : : : :
Qy 47 SSVTKSNGLLNITFKYDNCTPILNSVGHVIGDVQNTISQYACVEQVAVTILWTANAIG 106
Db : : : : :
Qy 119 IEFUKGRFVILIELKSEGRQCOQILKDPKOLNSSFKRTGMESQPFANMKPFTDIFYVKV 178
Db : : : : :
Qy 107 IEYLGRFVILIELKSEGRQCOQVLRDPKOLSPSFRTGMESNPPFANLKPFTDIFYVKIV 166
Qy 179 PFPISKESNYHPFFRTRACDLILQDNLACKFPWKPRNLNLSQHSMDQVSDHAPHN 238
Db : : : : :
Qy 167 PFPISKESNYHPFFRTRPCELLQENLICKYWKPRNLNVTQOGFNQVSDHAPHN 226
Qy 239 FGRFFYLHYLKHGEPFKRTCKOBTETTSCLLQNVSPGDYIELVDDTNTTRKVMH 298
Db : : : : :
Qy 227 FGRFFYLHYLKHGEPFKRTCKOBTETTSCLLQNVSPGDYIELVDDTNTTRKVMH 286
Qy 299 YALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKRKKQENIYSHLDEESSESYT 358
Db : : : : :
Qy 287 YALKPVHSPWAGPIRAITVPLVVISAFATLFTVMCKRKKQENIYSHLDEESSESYA 346
Qy 359 AALPRERLRPRPKVFLCYSSKDGQNHMVVOCFAYFLQDFCGCEVALDLWEDFSLCREG 418
Db : : : : :
Qy 347 AGLPVERLRPRPKVFLCYSSKDCQKHINVIQCFAYFLQDFCGCEVALDLWEDLKICKES 406
Qy 419 REWIOKIHESQFIIVVCSKGMKYFVDKKNYKHGGRGSGKGLFLVAVSAIAEKLROA 478
Db : : : : :
Qy 407 KEMWIKKINESQFIIVVCSKGMKYFVEKKNYKHGGRGSGKGLFLVAVSAIAEKLROA 466
Qy 479 KQSSAALSFKIYAVFYDSCGDPVGLDLSKYRLMDNLPLQCSHLHSRDHGLQEPGQH 538
Db : : : : :
Qy 467 KQNSN-DLCKFIYAVFYDSCGDPVGLDLSKYRLMDNLPLQCSHLHSRDHGLQEPG 525
Qy 539 TRQSRNRYFRSKGRSLYVAICNMHQFIDEPDMFEKQFVFPHPPLRYREPVLKEDFS 598
Db : : : : :
Qy 526 PVNVSKRNYFRSKGRSLYVAICNMHQFIDEPDMFEKQFIPFLPHLYSEPVMEKFX 585
Qy 599 GLVLNDVNMCKPESDFCLKVEAAVLGATGAPDSQHSQHGGLDQGEARP-ALDGSAA 657
Db : : : : :
Qy 586 GLVLNDLVNKAADDDFYLKTVDVNIISA-GSSDSHCIIQHLNLGEDVETQDIQRGSSVL 644
Qy 658 QPLHTYKAGSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLG 717
Db : : : : :
Qy 645 RPLHVAKASNLKDMRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGLG 704
Qy 718 BEEPALPS-KLLSSGCKADLCGRSYTDELHAVAPL 753
Db : : : : :
Qy 705 BEEPVITSTKFLPGICKAELHCHHTDELQAIAPL 741

RESULT 9

Q8AV76 ID Q8AV76 PRELIMINARY; PRT; 697 AA.
AC Q8AV76;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sef protein (fragment).
GN Name=SEF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianineae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Facial mesenchyme;
RX MEDLINE=22651784; PubMed=12765832; DOI=10.1016/S0968-0004(03)00067-7;
RA Novatchkova M., Leibbrandt A., Wierzowa J., Neubueser A.,
RA Eisenhaber F.;
RT "The STIR-domain superfamily in signal transduction, development and
RT immunity".
RL Trends Biochem. Sci. 28:226-229(2003).
DR EMBL; AJ508679; CAD4845.1; -.

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
FT NON_TER 1
SQ SSEQUENCE 697 AA; 79259 MW; D288939B1727F2C3 CRC64;
Query Match 70.6%; Score 2834; DB 2; Length 697;
Best Local Similarity 75.5%; Pred. No. 1.6e-207;
Matches 528; Conservative 75; Mismatches 92; Indels 4; Gaps 4;
Qy 57 GVGPASRNSGLNITFKYDNCTTILNVPVGHVIADQNITISQYACHQDVAVTILMSPGA 116
Db : : : : :
Qy 117 LGTEFLKGRFVILIELKSEGRQCOQILKDPKOLNSSFKRTGMESQPFANMKPFTDIFYVK 176
Db : : : : :
Qy 61 IGTEYLRGRFVILIELKSEGRQCOQVLRDPKOLSPSFRTGMESNPPFANLKPFTDIFYVK 120
Qy 177 VVFPFISKESNYHPFFRTRACDLILQDNLACKFPWKPRNLNLSQHSMDQVSDHAPH 236
Db : : : : :
Qy 121 IVFPFISKESNYHPFFRTRPCELLQENLICKYWKPRNLNVTQOGFNQVSDHAPH 180
Qy 237 HNFGRFFYLHYLKHGEPFKRTCKOBTETTSCLLQNVSPGDYIELVDDTNTTRKV 296
Db : : : : :
Qy 181 HNFGRFFYLHYLKHGEPFKRTCKOBTETTSCLLQNVSPGDYIELVDDTNTTRKT 240
Qy 297 MYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCKRKKQENIYSHLDEESSEST 356
Db : : : : :
Qy 241 MYALKPVHSPWAGPIRAITVPLVVISAFATLFTVMCKRKKQENIYSHLDEESSESA 300
Qy 357 YTAALPRERLRPRPKVFLCYSSKDGQNHMVVOCFAYFLQDFCGCEVALDLWEDFSLCRE 416
Db : : : : :
Qy 301 YGAGLPVERLRPRPKVFLCYSSKDCQKHINVIQCFAYFLQDFCGCEVALDLWEDLKICK 360
Qy 417 GOREWIOKIHESQFIIVVCSKGMKYFVDKKNYKHGGRGSGKGLFLVAVSAIAEKLRL 476
Db : : : : :
Qy 361 SQKWLIIKINESQFIIVVCSKGMKYFVEKKNYKHGGRGSGKGLFLVAVSAIAEKLRL 420
Qy 477 QAKOSSAALSFKIYAVFYDSCGDPVGLDLSKYRLMDNLPLQCSHLHSRDHGLQEPG 536
Db : : : : :
Qy 421 QAKQNSN-DLCKFIYAVFYDSCGDPVGLDLSKYRLMDNLPLQCSHLHSRDHGLQEPG 479
Qy 537 QHTRQSRNRYFRSKGRSLYVAICNMHQFIDEPDMFEKQFVFPHPPLRYREPVLKEDF 596
Db : : : : :
Qy 480 VFPNVSKRNYFRSKGRSLYVAICNMHQFIDEPDMFEKQFIPFLPHLYSEPVMEKFX 539
Qy 597 DSGLVNDVNMCKPESDFCLKVEAAVLGATGAPDSQHSQHGGLDQGEARPALD-GSA 655
Db : : : : :
Qy 540 DSGLVNDLVNKAADDDFYLKTVDVNIISA-GSSDSHCIIQHLNLGEDVETQDIQSGSS 598
Qy 656 ALQPLHTYKAGSPDMRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSSG 715
Db : : : : :
Qy 599 VLRLPLHVAKASNLKDMRDSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSSG 658
Qy 716 LGBEEPPALPS-KLLSSGCKADLCGRSYTDELHAVAPL 753
Db : : : : :
Qy 659 LGBEEPPVITSTKFLPGICKAELHCHHTDELQAIAPL 697

RESULT 10

Q8K447 ID Q8K447 PRELIMINARY; PRT; 594 AA.
AC Q8K447;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein short form.
GN Name=Il17rd; Synonyms=Il17rlm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=1295813; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "Self inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
DR EMBL: AF494209; AAM74078.1; -
DR MGD; MGI:2159727; I117rd.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Receptor.
SQ SEQUENCE 594 AA; 66780 MW; EABEG655DC4EC3 CRC64;

Query Match 66.7%; Score 2675.5; DB 2; Length 594;
Best Local Similarity 84.8%; Pred. No. 1.6e-195;
Matches 507; Conservative 34; Mismatches 50; Indels 7; Gaps 4;

QY 159 MESQFFLNKPEFDYFKVYVFPFSSIKNESNYHFFFRTRACDLLQPNLACKPFWKPRN 218
DB 1 MESQFFLNKPEFDYFKVYVFPFSSIKNESNYHFFFRTRACDLLQPNLACKPFWKPRN 60

QY 219 LNIHQSDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRKTCQEQTTTSCLLQNV 278
DB 61 LNIHQSDMHVSDHAPHNFGFRFFYLHYKLKHEGPFKRKTCQEQTTTSCLLQNV 120

QY 279 PGDYIIELVDNTNTRKVMHYALPVKSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 338
DB 121 PGDYIIELVDNTNTRKAAQVVKVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180

QY 339 QQENIYSHLDESSESSYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDF 398
DB 181 QQENIYSHLDESSESSYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDF 240

QY 399 CGCEVALDLWDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRGS 458
DB 241 CGCEVALDLWDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRGS 300

QY 459 KGGEFLVAVSAIAEKLQAKSSAALSKFIIVFYDSCGDVPGILDSTKRLMDNL 518
DB 301 AQGEFFLVAVAAIAEKLQAKSSAALSKFIIVFYDSCGDVPGILDSTKRLMDNL 360

QY 519 POLCSHLHSRDHGLQEP-CQHTROGSRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 577
DB 361 PELCAHLHS---GQEVLGQHPGHSSRRNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 417

QY 578 FVPHPPLRYREPVLKFDGLVNDVCMCKPGPESDFCLKVEAAVLGATPADSOH--E 635
DB 418 FIPFQHPPLRYREPVLKFDGLVNDVCMCKPGPESDFCLKVEAAVLGATPADSOH--E 477

QY 636 SQHGLDQDGEARPAIDGSAALQPLLTHTVYKAGSPDMRDSGIYDSSVPSSLSPLMEG 695
DB 478 SQHGLDQDGEARPAIDGSAALQPLLTHTVYKAGSPDMRDSGIYDSSVPSSLSPLMEG 537

QY 696 LSTDTQETSSLTSSVSSSGLGEPPALPKLLSSGCKADLGCSTYDELHVAAPL 753
DB 538 LSPDQIETSSLTSSVSSSGLGEPPALPKLLSSGCKADLGCSTYDELHVAAPL 594

RESULT 11
Q8R5J8 ID Q8R5J8 PRELIMINARY; PRT; 582 AA.
AC Q8R5J8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE Similar expression to FGF protein (Fragment).
GN Name=I117rd; Synonyms=Seif;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1824237; PubMed=11802165; DOI=10.1038/ncb750;
RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
RT "Seif is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signalling.";
RL Nat. Cell Biol. 4:170-174(2002).
DR EMBL; AF424804; AAL79530.1; -
DR MGD; MGI:2159727; I117rd.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
FT NON_TER 1
SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 65.2%; Score 2616.5; DB 2; Length 582;
Best Local Similarity 84.6%; Pred. No. 5.1e-191;
Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

QY 171 TDYFVKVVPFSSIKNESNYHFFFRTRACDLLQPNLACKPFWKPRNLISQHSMDV 230
DB 1 TDYFVKVVPFSSIKNESNYHFFFRTRACDLLQPNLACKPFWKPRNLISQHSMDV 60

QY 231 SPDHAPHNFGFRFFYLHYKLKHEGPFKRKTCQEQTTTSCLLQNVSPGDYIIELVDNT 290
DB 61 SPDHAPHNFGFRFFYLHYKLKHEGPFKRKTCQEQTTTSCLLQNVSPGDYIIELVDNT 120

QY 291 NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 350
DB 121 NTRKAAQVVKVSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 180

QY 351 SSESSTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDFCGCEVALDLWED 410
DB 181 SPESSTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVOCFAIFLQDFCGCEVALDLWED 240

QY 411 FSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGEFLVAVSA 470
DB 241 FSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGEFLVAVSA 300

QY 471 IAEKLQAKSSAALSKFIIVFYDSCGDVPGILDSTKRLMDNLPCSLHLSRDH 530
DB 301 IAEKLQAKSSAALSKFIIVFYDSCGDVPGILDSTKRLMDNLPCSLHLSRDH 357

QY 531 GLQEP-CQHTROGSRNNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVPHPPPLRYR 589
DB 358 GEQEVLGQHPGHSSRRNYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVPHPPPLRYR 417

QY 590 EPVLKFDGLVNDVCMCKPGPESDFCLKVEAAVLGATPADSOH--ESQHGGLDQDGEA 647
DB 418 EPVLKFDGLVNDVCMCKPGPESDFCLKVEAAVLGATPADSOH--ESQHGGLDQDGEA 477

QY 648 RPALDGSNAALQPLLTHTVYKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLT 707
DB 478 QPSCDSAPALQPLLTHTVYKAGSPDMRDSGIYDSSVPSSLSPLMEGLSTDTQETSSLT 537

QY 708 ESVSSSSGLGEEPPALPKLLSSGCKADLGCSTYDELHVAAPL 753
DB 538 ESVSSSSGLGEEPPALPKLLSSGCKADLGCSTYDELHVAAPL 582
```

RESULT 12
Q8QHJ9

Db 464 SAIISEKLKVEHQSS-DLSRFMSVYFDYSHETDVTSLSLAPKFLMDQLPQLFARLHS 522

Qy 528 RDHGLQEPGQHTQGRSRRNYSKGRSLYVAICNMHQFIDEEDWPEKQFVPPHPPPLR 587

Db 523 RQLSLTREPQPPNVNKRNYFCSKGRSLYVAIYNMHQVTOEPDWLEKELM---PPPLP 579

Qy 588 YREPVLEKFGSLVINDVMCKPGPESDFCLKVEAAVL-----GATGPADQSHEHQGG 640

Db 580 NKRTPEKVDGLVNEVKLKHGSESE-CPVRSNVLLIPQTPGVGVSLSLSRDLGEGS 638

Qy 641 LDQGEARPALDGAALQPLHTVKAGSPSPMDPRDSGLYDSSVPSSELSPLMEGLSTDQ 700

Db 639 SSQD-----AGSCRPLVHTDGSAPPMPRDRDSGLYDSSVPSSELSPLMDGLSPDH 689

Qy 701 TETSLTESVSSSGLEGEPPALPSKLLSSGS-CKADL 738

Db 690 ADNSSLADSVSSSGLGDEEPPAVSSLLHCTAHTICKADL 728

RESULT 14

Q8HXE8 PRELIMINARY; PRT; 109 AA.

AC Q8HXE8

DT 01-MAR-2003 (TREMREL. 23, Created)

DT 01-MAR-2003 (TREMREL. 23, Last sequence update)

DT 01-MAR-2003 (TREMREL. 23, Last annotation update)

DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Frontal lobe left;

RX MEDLINE=21459551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,

RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;

RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human

RT chromosomes.";

RL Gene 275:31-37(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Frontal lobe left;

RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB093642; BAC21616.1; -

KW Hypothetical protein.

QY SEQUENCE 109 AA; 11609 MW; 7EB13B49DB4C925B CRC64;

Query Match 13.4%; Score 538; DB 2; Length 109;

Best Local Similarity 87.2%; Pred. No. 2.9e-33;

Matches 102; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

QY 1 MAPWLQLCSVFTVNAVLGSLQSLAVAGSGRGARGADTCGRWKAARPRLCVANGVGP 60

Db 1 MAPWLQLCSVFTVNAVLGSLQSLAVAGSGRGARGADTCGRW-----GVGP 46

QY 61 ASRNSGLNYNITPKYDNTTYLNPVGHVIAADQNTISQYACHQDVAVTILMSPGAL 117

Db 47 ASRNSGLNYNITPKYDNTTYLNPVGHVIAADQNTISQYACHQDVAVTILMSPGVL 103

RESULT 15

IL17R_HUMAN

ID IL17R_HUMAN STANDARD; PRT; 866 AA.

AC Q96F46; O43844;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Interleukin-17 receptor precursor (IL-17 receptor).

GN Name=IL17R;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=T-cell;

RX MEDLINE=98035683; PubMed=9367539; DOI=10.1006/cyto.1997.0240;

RA Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,

RA Vanden Bos T., Zappone J., Painter S.L., Armitage R.J.;

RT "Molecular characterization of the human interleukin (IL)-17

RT receptor.";

RL Cytokine 9:794-800(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.B.,

RA Schnerch A., Schein J.E., Jones S.J.M., Maxra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP SEQUENCE OF 33-47.

RX PubMed=15340161; DOI=10.1110/ps.04682504;

RA Zhang Z., Henzel W.J.;

RT "Signal peptide prediction based on analysis of experimentally

RT verified cleavage sites.";

RL Protein Sci. 13:2819-2824(2004).

CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,

CC suggesting that additional components are involved in IL17-induced

CC signaling.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Widely expressed.

CC -!- PTM: Glycosylated.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

DR EMBL; U58917; AAB99730.1; -

DR EMBL; BC011624; AAH11624.1; -

DR Genew; HGNC:5985; IL17R.

DR H-InvDB; HIX0016207; -

DR MiMi; 605461; -

DR GO; GO:0005887; C: integral to plasma membrane; NAS.

DR GO; GO:0030368; F: interleukin-17 receptor activity; NAS.

DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . ; NAS.

KW Direct protein sequencing; Glycoprotein; Receptor; Signal;

KW Transmembrane.

FT SIGNAL 1 32 Interleukin-17 receptor.

FT CHAIN 33 866 Extracellular (potential).

FT DOMAIN 33 320 Potential.

FT TRANSMEM 321 341

FT DOMAIN 342 866 Cytoplasmic (potential).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:33:31 ; Search time 116.169 Seconds
(without alignments)
2390.439 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRMKAAARPRLCVAN.....CKADLGCRSYTDLHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 3829 | 100.0 | 753 | 5 | ABB07626 Human cyt |
| 2 | 3819 | 99.7 | 753 | 5 | ABB07627 Human cyt |
| 3 | 3741 | 97.7 | 739 | 5 | ABB07628 Human cyt |
| 4 | 3725 | 97.3 | 738 | 4 | Aau09904 Human Int |
| 5 | 3721 | 97.2 | 738 | 4 | Aau09953 Human Int |
| 6 | 3720 | 97.2 | 738 | 4 | Aau09954 Human Int |
| 7 | 3718 | 97.1 | 738 | 4 | Aau09951 Human Int |
| 8 | 3718 | 97.1 | 738 | 4 | Aau09952 Human Int |
| 9 | 3718 | 97.1 | 738 | 4 | Aau09956 Human Int |
| 10 | 3714 | 97.0 | 738 | 4 | Aau09957 Human Int |
| 11 | 3714 | 97.0 | 738 | 4 | Aau09955 Human Int |
| 12 | 3708 | 96.8 | 728 | 7 | ADB65245 Human pro |
| 13 | 3703 | 96.7 | 728 | 4 | Aau04958 Human Int |
| 14 | 3703 | 96.7 | 728 | 6 | ABU89705 Human Int |
| 15 | 3703 | 96.7 | 728 | 6 | ABU72600 Human IL- |
| 16 | 3703 | 96.7 | 728 | 6 | ADA43241 Human Int |
| 17 | 3703 | 96.7 | 728 | 7 | ADA49782 Human Int |
| 18 | 3703 | 96.7 | 728 | 7 | ADA26975 Human PRO |
| 19 | 3703 | 96.7 | 728 | 7 | ADB66909 Human PRO |
| 20 | 3703 | 96.7 | 728 | 7 | ABW02061 Human IL- |
| 21 | 3703 | 96.7 | 728 | 7 | ADG87393 Human PRO |
| 22 | 3703 | 96.7 | 728 | 7 | ADL16689 Human PRO |
| 23 | 3703 | 96.7 | 728 | 8 | ADL16650 Human PRO |
| 24 | 3703 | 96.7 | 728 | 8 | ADL171310 Human IL- |
| 25 | 3700 | 96.6 | 739 | 4 | Aau10602 Human Int |

ALIGNMENTS

RESULT 1

ABB07626

ID ABB07626 standard; protein; 753 AA.

XX ABB07626;

DT 20-MAY-2002 (first entry)

DE Human cytokine receptor, Zcytor18 amino acid sequence.

XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumour;
XX erythroleukemia; chromosome 3p14.3; gene therapy.

OS Homo sapiens.

XX WO200208259-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023253.

XX 26-JUL-2000; 2000US-0220747P.

XX (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

XX WPI; 2002-217048/27.

XX N-PSDB; ABA95031, ABA95032.

XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 1; Page 2; 119pp; English.

XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumour growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 3657.5 | 95.5 | 738 | 5 | AAU11355 | Aau11355 Human DNA |
| 27 | 3208 | 83.8 | 739 | 5 | ABB07630 | Abb07630 Murine cy |
| 28 | 3176 | 82.9 | 595 | 6 | AAE33485 | Aae33485 Human REM |
| 29 | 3170 | 82.8 | 595 | 4 | ABUS3091 | Abu3091 Human tra |
| 30 | 3166 | 82.7 | 595 | 5 | ABP69026 | Abp69026 Human pol |
| 31 | 2515.5 | 65.7 | 554 | 5 | AAU91330 | Aau91330 Human nov |
| 32 | 1334 | 34.8 | 296 | 4 | AAU10601 | Aau10601 5' portio |
| 33 | 312 | 8.1 | 866 | 2 | AAW04185 | Aaw04185 Human int |
| 34 | 312 | 8.1 | 866 | 2 | AAW61272 | Aaw61272 Human int |
| 35 | 312 | 8.1 | 866 | 2 | AAW92409 | Aaw92409 Human IL- |
| 36 | 312 | 8.1 | 866 | 3 | AAU97131 | Aau97131 Human int |
| 37 | 312 | 8.1 | 866 | 3 | AAU97181 | Aau97181 Human int |
| 38 | 312 | 8.1 | 866 | 3 | AAU03807 | Aau03807 Human int |
| 39 | 312 | 8.1 | 866 | 3 | AAU99941 | Aau99941 Human IL- |
| 40 | 312 | 8.1 | 866 | 4 | AAU62066 | Aau62066 Human IL- |
| 41 | 312 | 8.1 | 866 | 4 | AAU72754 | Aau72754 Human int |
| 42 | 312 | 8.1 | 866 | 5 | ABB78079 | Abb78079 Amino aci |
| 43 | 312 | 8.1 | 866 | 7 | ADD25546 | Ad25546 Binding d |
| 44 | 312 | 8.1 | 866 | 8 | ADJ88265 | Adj88265 Human IL- |
| 45 | 312 | 8.1 | 866 | 8 | ADL24269 | Adl24269 Human IL- |

CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 amino acid sequence
XX
SQ Sequence 753 AA;
Query Match 100.0%; Score 3829; DB 5; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAQNI 60
Db 36 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAQNI 95
Qy 61 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSFFK 120
Db 96 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSFFK 155
Qy 121 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 180
Db 156 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 215
Qy 181 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYLKLKHEGPFKRKTCKQEQTTETTSCLLQ 240
Db 216 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYLKLKHEGPFKRKTCKQEQTTETTSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
Qy 301 RKQQENIYSHLDESSSESTYTAALPRRLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
Db 336 RKQQENIYSHLDESSSESTYTAALPRRLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
Qy 361 QDFCCEVALDLMEDFSLCREGQEWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db 396 QDFCCEVALDLMEDFSLCREGQEWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 455
Qy 421 RGSKGELFLVAVSAIAEKLQAKOSSAALSKEFIIVFYDYSCEGDVPGIILDLSTKYRLM 480
Db 456 RGSKGELFLVAVSAIAEKLQAKOSSAALSKEFIIVFYDYSCEGDVPGIILDLSTKYRLM 515
Qy 481 DNLPLCSSLHSHRDHGLQEPGQHTROGSRNRYFSKGRSLYVAICNWHQFIDSEPDWEE 540
Db 516 DNLPLCSSLHSHRDHGLQEPGQHTROGSRNRYFSKGRSLYVAICNWHQFIDSEPDWEE 575
Qy 541 KQFVFPFPPPLRYREPVLKEFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 600
Db 576 KQFVFPFPPPLRYREPVLKEFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE 635
Qy 601 SOHGGLDQDGEARPALDGSAAQLPLHTVTKAGSPDMPRDSGIYDSSVPSELSLPLMEG 660
Db 636 SOHGGLDQDGEARPALDGSAAQLPLHTVTKAGSPDMPRDSGIYDSSVPSELSLPLMEG 695
Qy 661 LSTQDTETSSLTESVSSSGSGEPEPPALPSKLLSSGCKADLCRSYTDDELHAVAPL 718
Db 696 LSTQDTETSSLTESVSSSGSGEPEPPALPSKLLSSGCKADLCRSYTDDELHAVAPL 753
RESULT 2
ABB07627
ID ABB07627 standard; protein; 753 AA.
XX
AC ABB07627;
XX
XX
DT 20-MAY-2002 (first entry)
XX
XX Human cytokine receptor, Zcytor18 variant sequence.
DE
XX
XX Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; variant.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 269 /label= T269M
FT /note= "wild-type Thr is replaced with Met"
FT Misc-difference 750 /label= V750A
FT /note= "wild-type Val is replaced with Ala"
XX
XX WO200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-US023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, Kuestner RE, Gao Z;
XX WPI; 2002-217048/27.
XX N-PSDB; ABA95033, ABA95034.
XX
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX
XX Disclosure; Page 94-98; 119pp; English.
XX
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumour growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 variant amino acid sequence
SQ Sequence 753 AA;
Query Match 99.7%; Score 3819; DB 5; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAQNI 60
Db 36 ADTCGWRMKAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAQNI 95
Qy 61 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSFFK 120
Db 96 TISQYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCQQLILKDPKQLNSFFK 155
Qy 121 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 180
Db 156 RTGMESQPFLLNMKFETDYFKVVPFPSPISKNESNYHPFFRTRACDILLQDNLACKPFWK 215
Qy 181 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYLKLKHEGPFKRKTCKQEQTTETTSCLLQ 240
Db 216 PRNLNISQHGSDMQVSPFDHAPHNFGFRFFYLHYLKLKHEGPFKRKTCKQEQTTETTSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
Qy 301 RKQQENIYSHLDESSSESTYTAALPRRLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360

|||||
336 RKQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
QY 361 QDFCGCEVALDLWEDFSICREGQEWIQTTHESQFIIVVCSKGMKYFVDKKNYKHGGG 420
Db 396 QDFCGCEVALDLWEDFSICREGQEWIQTTHESQFIIVVCSKGMKYFVDKKNYKHGGG 455
QY 421 RSGKGELFLVAVSAIAEKLQAKQSSAALSKEFIAYVFDYSCGDPVPGILDSTKYRLM 480
Db 456 RSGKGELFLVAVSAIAEKLQAKQSSAALSKEFIAYVFDYSCGDPVPGILDSTKYRLM 515
QY 481 DNLQOLCSHLHSRDHGLQEPQCHTRQGSRRNYFRSKGRSLYVAICNMHQFIDEPDWFE 540
Db 516 DNLQOLCSHLHSRDHGLQEPQCHTRQGSRRNYFRSKGRSLYVAICNMHQFIDEPDWFE 575
QY 541 KQFVFPFPPPLRYREPVLKEDSGVLVNDVCKPSPESDFCLKVEAAVLGATGADSOHE 600
Db 576 KQFVFPFPPPLRYREPVLKEDSGVLVNDVCKPSPESDFCLKVEAAVLGATGADSOHE 635
QY 601 SOHGLDQDGEARPDGSAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 660
Db 636 SOHGLDQDGEARPDGSAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 695
QY 661 LSTDQTETSSITESVSSSGIGEEPPALPSKLLSSGCKADLCGRSYTDELHAAVPL 718
Db 696 LSTDQTETSSITESVSSSGIGEEPPALPSKLLSSGCKADLCGRSYTDELHAAVPL 753

RESULT 3
ABB07628
ID ABB07628 standard; protein; 739 AA.
XX AC ABB07628;
XX DT 20-MAY-2002 (first entry)
XX DE Human cytokine receptor, Zcytor18 splice variant.
XX KW Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
KW pulmonary alveolar proteinosis; familial periodic fever; antitumour;
KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
XX OS Homo sapiens.
XX PN WO200208259-A2.
XX PD 31-JAN-2002.
XX PF 23-JUL-2001; 2001WO-US023253.
XX PR 26-JUL-2000; 2000US-0220747P.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Presnell SR, Kuestner RE, Gao Z;
XX WPI; 2002-217048/27.
XX DR N-PSDB; ABA95035, ABA95036.
XX PT New cytokine receptor polypeptide designated zcytor18, useful for
PT inhibiting cell proliferation associated with psoriasis or tumor growth,
PT and modulating immune system by binding to endogenous zcytor18 ligand.
XX PS Claim 1; Page 102-106; 119pp; English.

CC The invention relates to an isolated cytokine receptor polypeptide
CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
CC standard recombinant methodology. The polypeptides can be used to inhibit
CC cell proliferation associated with psoriasis or tumour growth. The
CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are

CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 splice variant
XX SQ Sequence 739 AA;
Query Match 97.7%; Score 3741; DB 5; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;
QY 1 ADTCGWRKMAAARPRLCVANEVGPASRNSGLNITFKYDNCITTYLNPVGHVITADAQNI 60
Db 36 ADTCGWR-----GVGPASRNSGLNITFKYDNCITTYLNPVGHVITADAQNI 81
QY 61 TISQYACHDOVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKQINSFVK 120
Db 82 TISQYACHDOVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKQINSFVK 141
QY 121 RTGMESQPFNLNMPETDYFKVAVPFPFSIKNESNYHFFFRTRACDILLQDNLACKPFWK 180
Db 142 RTGMESQPFNLNMPETDYFKVAVPFPFSIKNESNYHFFFRTRACDILLQDNLACKPFWK 201
QY 181 PRNLNISQHSQDMQVSFDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQTETTSCLLQ 240
Db 202 PRNLNISQHSQDMQVSFDHAPHNFGFRFFYLHYLKHGEPFKRTCKOEQTETTSCLLQ 261
QY 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 262 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
QY 301 RKQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
Db 322 RKQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 381
QY 361 QDFCGCEVALDLWEDFSICREGQEWIQTTHESQFIIVVCSKGMKYFVDKKNYKHGGG 420
Db 382 QDFCGCEVALDLWEDFSICREGQEWIQTTHESQFIIVVCSKGMKYFVDKKNYKHGGG 441
QY 421 RSGKGELFLVAVSAIAEKLQAKQSSAALSKEFIAYVFDYSCGDPVPGILDSTKYRLM 480
Db 442 RSGKGELFLVAVSAIAEKLQAKQSSAALSKEFIAYVFDYSCGDPVPGILDSTKYRLM 501
QY 481 DNLQOLCSHLHSRDHGLQEPQCHTRQGSRRNYFRSKGRSLYVAICNMHQFIDEPDWFE 540
Db 502 DNLQOLCSHLHSRDHGLQEPQCHTRQGSRRNYFRSKGRSLYVAICNMHQFIDEPDWFE 561
QY 541 KQFVFPFPPPLRYREPVLKEDSGVLVNDVCKPSPESDFCLKVEAAVLGATGADSOHE 600
Db 562 KQFVFPFPPPLRYREPVLKEDSGVLVNDVCKPSPESDFCLKVEAAVLGATGADSOHE 621
QY 601 SOHGLDQDGEARPDGSAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 660
Db 622 SOHGLDQDGEARPDGSAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 681
QY 661 LSTDQTETSSITESVSSSGIGEEPPALPSKLLSSGCKADLCGRSYTDELHAAVPL 718
Db 682 LSTDQTETSSITESVSSSGIGEEPPALPSKLLSSGCKADLCGRSYTDELHAAVPL 739

RESULT 4
AAU09904
ID AAU09904 standard; protein; 738 AA.
XX AC AAU09904;
XX DT 14-FEB-2002 (first entry)
XX DE Human Interleukin 17 (hIL-17) receptor like protein.
XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;

anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial; hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian; anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic; vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological; hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease; bone disease; vascular disorder; eye disorder; cancer; human.

Homo sapiens.

WO200168859-A2.

20-SEP-2001.

15-MAR-2001; 2001WO-US008678.

16-MAR-2000; 2000US-0189816P.

28-NOV-2000; 2000US-00724460.

(AMGE-) AMGEN INC.

Jing S;

WPI; 2001-611392/70.

N-PSDB; AAS15346.

Nucleic acids encoding interleukin 17 receptor like polypeptides, useful for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.

Claim 2; Page 152-154; 158pp; English.

The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also be used as diagnostic probes to detect and quantify the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human Interleukin 17 (IL-17) receptor like protein described in the method of the invention

Sequence 738 AA;

Query Match 97.3%; Score 3725; DB 4; Length 738;
Best Local Similarity 97.8%; Pred. NO. 0;
Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTGGRMKAAARPRICVANEGVGASRNSGLYNTFKYDNCCTYLPVKGHVIAQAQNIIT 61
| | | | |
Db 37 DTGGRM-----GVGASRNSGLYNTFKYDNCCTYLPVKGHVIAQAQNIIT 82
| | | | |

Qy 62 ISQYACHDQAVTILWSPGALGIFBLKGFVRVILEELKSEGRQCQQLIKDPKQLNSSFKR 121
| | | | |
Db 83 ISQYACHDQAVTILWSPGALGIFBLKGFVRVILEELKSEGRQCQQLIKDPKQLNSSFKR 142
| | | | |

Qy 122 TGMESOPFLNMKETDYFVKVVPFPSPSIKNESNYHPFFRTRACDLLLPDNLACKPWP 181
| | | | |
Db 143 TGMESQPFLLNMKETDYFVKVVPFPSPSIKNESNYHPFFRTRACDLLLPDNLACKPWP 202
| | | | |
Qy 182 RNLNI SQHSDMQVSPDHAPHNFGFRFFYLHYLKHGEPFKRTCKQEQTTTSCLLQN 241
| | | | |
Db 203 RNLNISQHSDMQVSPDHAPHNFGFRFFYLHYLKHGEPFKRTCKQEQTTTSCLLQN 262
| | | | |
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVNCR 301
| | | | |
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVNCR 322
| | | | |
Qy 302 KKOENIYSHLDESSSESYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCFAYFLQ 361
| | | | |
Db 323 KKOENIYSHLDESSSESYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCFAYFLQ 382
| | | | |
Qy 362 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
| | | | |
Db 383 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
| | | | |
Qy 422 GSGKGELFLVAVSAIAEKLRQAKQSSAALSKEIAYFYDSCGDPVGIILDLSTKYFLMD 481
| | | | |
Db 443 GSGKGELFLVAVSAIAEKLRQAKQSSAALSKEIAYFYDSCGDPVGIILDLSTKYFLMD 502
| | | | |
Qy 482 NLPOLCSHLHSDRHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNNHQFIDEPDWFEK 541
| | | | |
Db 503 NLPOLCSHLHSDRHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNNHQFIDEPDWFEK 562
| | | | |
Qy 542 QFVFPHPPLRYREPVLKFDGLVLDNMVCKFGPESDFCLKVEAAVLGATGSPADSQHS 601
| | | | |
Db 563 QFVFPHPPLRYREPVLKFDGLVLDNMVCKFGPESDFCLKVEAPVLGATGSPADSQHS 622
| | | | |
Qy 602 QHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMRPDSGIYDSSVPSSELSLPLMEGL 661
| | | | |
Db 623 QHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMRPDSGIYDSSVPSSELSLPLMEGL 682
| | | | |
Qy 662 STDQTTSSLTESVSSSGSGEPEPPALPSKLLSSGCKADLGCSTYDELHVAAP 717
| | | | |
Db 683 STDQTTSSLTESVSSSGSGEPEPPALPSKLLSSGCKADLGCSTYDELHVAAP 738
| | | | |

RESULT 5
AAU09953
ID AAU09953 standard; protein; 738 AA.
XX
AC AAU09953;
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 363
FT /label= Ser, Thr, Ala, Cys
XX
FN WO200168859-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-US008678.


```
PS Claim 21; Page; 158pp; English.
XX
CC The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicaemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17rlp may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17rlp antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 21
XX
SQ Sequence 738 AA;

Query Match          97.2%; Score 3720; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY 2 DTCGWRKMAARPLCVANEGVGPASRNSGLYNTFKYDNCNTTYLNPVGKHVIADAQNIT 61
DB |||||
DB 37 DTCGWR-----CGVGPASRNSGLYNTFKYDNCNTTYLNPVGKHVIADAQNIT 82

QY 62 ISQYACHDOVAVTILSPGALGIEFLGFRVILELSEGGQCOOLILKDPKQLNSFFKR 121
DB |||||
DB 83 ISQYACHDOQVAVTILSPGALGIEFLGFRVILELSEGGQCOOLILKDPKQLNSFFKR 142

QY 122 TGMESQPFLLNKFETDVFVKVVPFPIKVESNYHFFFRTRACDLLQPDNLACKPFWKP 181
DB |||||
DB 143 TGMESQPFLLNKFETDVFVKVVPFPIKVESNYHFFFRTRACDLLQPDNLACKPFWKP 202

QY 182 RNLNISQHSQDMQVSFDHAPNFGFRFPYLHYLKHGEPFKRKTCKQEQTTTSCLLQN 241
DB |||||
DB 203 RNLNISQHSQDMQVSFDHAPNFGFRFPYLHYLKHGEPFKRKTCKQEQTTTSCLLQN 262

QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTWCR 301
DB |||||
DB 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTWCR 322

QY 302 KQQENIYSHLDESSSSTYTAALPRERLPRPKVFLCYSSKDGQNHMNVVQCFAFLQ 361
DB |||||
DB 323 KQQENIYSHLDESSSSTYTAALPRERLPRPKVFLCYSSKDGQNHMNVVQCFAFLQ 382

QY 362 DFCCEVALDWEFSLCREGQREBWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
DB |||||
DB 383 DFCCEVALDWEFSLCREGQREBWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442

QY 422 GSGGGEFLVAVSAIAEKLRAKQSSAALSKEFTAVVFDYCEGDVPGILDLSKYRLMD 481
DB |||||
DB 443 GSGGGEFLVAVSAIAEKLRAKQSSAALSKEFTAVVFDYCEGDVPGILDLSKYRLMD 502

QY 482 NLPQLCSHLHSDHGLQPGQHTQGSRRNFRSKSGRSLVAICNMHQFIDEFPDWFKE 541
DB |||||
DB 503 NLPQLCSHLHSDHGLQPGQHTQGSRRNFRSKSGRSLVAICNMHQFIDEFPDWFKE 562
```

dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 18

XX
SQ Sequence 738 AA;

Query Match 97.1%; Score 3718; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

Qy 2 DTCGRMKAAARPLCVANEGVGPASRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 61
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 82

Qy 62 ISOYACHDQAVATILMSPGALGIEFLKGRVILBELKSEGRQCOOLILKDPKQNSSPFKR 121
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 142

Qy 83 ISOYACHDQAVATILMSPGALGIEFLKGRVILBELKSEGRQCOOLILKDPKQNSSPFKR 142
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 163

Qy 122 TGMESQPLNKKFTDFVKKVPPSPISKNESNYHFFRFRACDLLOPNLACKPFWKP 181
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 202

Qy 143 TGMESQPLNKKFTDFVKKVPPSPISKNESNYHFFRFRACDLLOPNLACKPFWKP 202
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 223

Qy 182 RNLNLSQHSQDMQVSDFAHNFGRFRFYHLHYKLKHEGPFKRTCKQEQTTTSCLLQN 241
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 262

Qy 203 RNLNLSQHSQDMQVSDFAHNFGRFRFYHLHYKLKHEGPFKRTCKQEQTTTSCLLQN 262
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 283

Qy 242 VSPGDYIIELVDDTNTTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAPATLFTVWCR 301
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 322

Qy 263 VSPGDYIIELVDDTNTTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAPATLFTVWCR 322
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 343

Qy 302 KQOENYSHLDESSSSTYTAALPRRLPRPKVFLCYSSKQGNHNVVQCFAYFLQ 361
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 382

Qy 323 KQOENYSHLDESSSSTYTAALPRRLPRPKVFLCYSSKQGNHNVVQCFAYFLQ 382
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 403

Qy 362 DFCGEVALDLWEDFSLCREGQREWVIOKHESQFIIVCSKGMKYFVDDKKNYKHGGGR 421
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 442

Qy 383 DFCGEVALDLWEDFSLCREGQREWVIOKHESQFIIVCSKGMKYFVDDKKNYKHGGGR 442
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 463

Qy 422 GSGKGEFLVAVSAIAEKLRAKQSSSAALSKFIIVFYDSCGDPGILDLSTKYRIMD 481
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 502

Qy 443 GSGKGEFLVAVSAIAEKLRAKQSSSAALSKFIIVFYDSCGDPGILDLSTKYRIMD 502
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 523

Qy 482 NLPQLCSHLHSDRDLQBPQGHQTRQGRNFRSKGSRSLVAVICNMHQIFDEPDWFEK 541
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 562

Qy 503 NLPQLCSHLHSDRDLQBPQGHQTRQGRNFRSKGSRSLVAVICNMHQIFDEPDWFEK 562
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 583

Qy 542 QFVFPHPPLRYRPLEVLEKPSGLVNDVMCKPGPESDFCLKVRAVLTGATGPDADSOHES 601
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 622

Qy 563 QFVFPHPPLRYRPLEVLEKPSGLVNDVMCKPGPESDFCLKVRAVLTGATGPDADSOHES 622
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 643

Qy 602 QHGLDQGEARPALDGSAAALQPLIHTVKAGSPSDMPRDSGIYDSSVPSSELSPLMBGL 661
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 682

Qy 623 QHGLDQGEARPALDGSAAALQPLIHTVKAGSPSDMPRDSGIYDSSVPSSELSPLMBGL 682
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 703

Qy 662 STDQTETSSLTSSVSSSSGLGEEEPALPSPKILSSGCKADLGCRSYDELHAVAP 717
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 738

Qy 683 STDQTETSSLTSSVSSSSGLGEEEPALPSPKILSSGCKADLGCRSYDELHAVAP 738
Db |||||-----GVXPSRNSGLYNTFKYDNCCTYVLPVGVHVIADAQNIT 759

RESULT 8
AAU09952
ID AAU09952 standard; protein; 738 AA.
XX
AC AAU09952;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #2.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr
FT
XX
XX
XX WO200168859-A2.
XX
PD 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008678.
XX
PR 16-MAR-2000; 2000US-0189816P.
PR 28-NOV-2000; 2000US-00724460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX
XX Claim 19; Page; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicaemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rp antibodies and antagonists may also be used to down regulate
XX expression and activity. Note: This sequence is not given in the

CC specification but is based on the human Interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 19
XX
SQ Sequence 738 AA;
Query Match 97.1%; Score 3718; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
Qy 2 DTCGRWKAARPLCVANEGVGPASNSGLYNTFKYDNCCTTLYNPVGKHVIADAQNIT 61
Db 37 DTCGWR-----GVGPASNSGLYNTFKYDNCCTTLYNPVGKHVIADAQNIT 82
Qy 62 ISQYACHDOAVTILMSPGALGIEFLKGRVILSELKSEGQCOOLILKOPKOLNSFKR 121
Db 83 ISQYACHDOAVTILMSPGALGIEFLKGRVILSELKSEGQCOOLILKOPKOLNSFKR 142
Qy 122 TGMESQPLNNKFTDYFVKVVPFPIKNSNYHPFFRTRACDILLQPNLACKPFWKP 181
Db 143 TGMESQPLNNKFTDYFVKVVPFPIKNSNYHPFFRTRACDILLQPNLACKPFWKP 202
Qy 182 RNLNISQHSQDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRTCKQEQTTTSCLLQN 241
Db 203 RNLNISQHSQDMQVSFDHAPHNFGFRFFYLHYKLKHEGPFKRTCKQEQTTTSCLLQN 262
Qy 242 VSPGDYIELVDDTNTTRKWHYALKPVHSPWAGPIRAVAITVPLVISAPATLFTVMCR 301
Db 263 VSPGDYIELVDDTNTTRKWHYALKPVHSPWAGPIRAVAITVPLVISAPATLFTVMCR 322
Qy 302 KQOENYSHLDESSSSTYTAALPRELRPRPKVFLCYSSKDGQNHMNVQCFAYFLQ 361
Db 323 KQOENYSHLDESSSSTYTAALPRELRPRPKVFLCYSSKDGQNHMNVQCFAYFLQ 382
Qy 362 DFCCEVALDLWEDFSLCREQREWVIQKIHESQFIIVVCSKGMKYFVKKNYKHGGGR 421
Db 383 DFCCEVALDLWEDFSLCREQREWVIQKIHESQFIIVVCSKGMKYFVKKNYKHGGGR 442
Qy 422 GSGGELFLVAVSAIAEKLRQAKOSSNAALSCKFTAVYDFYSCGQVPGILDLSKYRLMD 481
Db 443 GSGGELFLVAVSAIAEKLRQAKOSSNAALSCKFTAVYDFYSCGQVPGILDLSKYRLMD 502
Qy 482 NLPQLCSHLHSRDHGLQEPGQHTQGRSRNFRSKSGSLVVALCNHQFIDEPDWFEX 541
Db 503 NLPQLCSHLHSRDHGLQEPGQHTQGRSRNFRSKSGSLVVALCNHQFIDEPDWFEX 562
Qy 542 QFVFPHPPLRYRPFVLEKFDGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSQHE 601
Db 563 QFVFPHPPLRYRPFVLEKFDGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSQHE 622
Qy 602 QHGLDQGEARPALDGSAAALQPLHTVTKAGSPDMPRDSGIYDSSVPSSELSPLMEGL 661
Db 623 QHGLDQGEARPALDGSAAALQPLHTVTKAGSPDMPRDSGIYDSSVPSSELSPLMEGL 682
Qy 662 STDQTESLTSVSSSSGLGEERPPALPSKLLSGSKADLGRSRYTDELHAVAP 717
Db 683 STDQTESLTSVSSSSGLGEERPPALPSKLLSGSKADLGRSRYTDELHAVAP 738

RESULT 9
AAU09956
ID AAU09956 standard; protein; 738 AA.
XX
AC AAU09956;
XX
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #6.
XX

Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;

KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 515 /label= Asp, Glu
PN WO200168859-A2.
XX 20-SEP-2001.
XX 15-MAR-2001; 2001WO-US008678.
XX 16-MAR-2000; 2000US-0189816P.
XX 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX
XX Claim 23; Page; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicaemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity. Note: This sequence is not given in the
XX specification but is based on the human Interleukin 17 (IL-17) receptor
XX like protein sequence (AAU09904) and has been created according to
XX information given in claim 23
XX
SQ Sequence 738 AA;

Query Match 97.1%; Score 3718; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

Qy 2 DTCGRWKAARPLCVANEGVGPASNSGLYNTFKYDNCCTTLYNPVGKHVIADAQNIT 61
Db 37 DTCGWR-----GVGPASNSGLYNTFKYDNCCTTLYNPVGKHVIADAQNIT 82

QY 62 ISOVACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCOQLILKDPKQLNSSFKR 121
DB 83 ISOVACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCOQLILKDPKQLNSSFKR 142
QY 122 TGMESQPFLLNKKFTDYFKVVPFSPISKNESNYHPFFRTRACDILLIOPNLACKPFWKP 181
DB 143 TGMESQPFLLNKKFTDYFKVVPFSPISKNESNYHPFFRTRACDILLIOPNLACKPFWKP 202
QY 182 RNLNISQHGSDMOVSFOHAPHNFGFRFFYLHYKLKHEGPPKRTCKOQTETTSCLLQN 241
DB 203 RNLNISQHGSDMOVSFOHAPHNFGFRFFYLHYKLKHEGPPKRTCKOQTETTSCLLQN 262
QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 301
DB 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 322
QY 302 KKOQENYSHLDRESSSSTVTAALPRELRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
DB 323 KKOQENYSHLDRESSSSTVTAALPRELRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
QY 362 DFCCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHKGGR 421
DB 383 DFCCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHKGGR 442
QY 422 GSGKGLFLVAVSAIAEKLRQAKOSSAALSKFTAVFDYCEGDVPGILDSTKYRLMD 481
DB 443 GSGKGLFLVAVSAIAEKLRQAKOSSAALSKFTAVFDYCEGDVPGILDSTKYRLMD 502
QY 482 NLPQLCSHLHSDRHLQFPGQHTQGRSRRNYFRSKSGSLYVAICNMHQFIDEPPDWFPEK 541
DB 503 NLPQLCSHLHSDRHLQFPGQHTQGRSRRNYFRSKSGSLYVAICNMHQFIDEPPDWFPEK 562
QY 542 QFVFPHPPLRYRBPVLEKPSGLVNDVMCKPGPESDFCLKVEAPVILGATGPDADSOHES 601
DB 563 QFVFPHPPLRYRBPVLEKPSGLVNDVMCKPGPESDFCLKVEAPVILGATGPDADSOHES 622
QY 602 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPDRDSGLYDSSVPSSELSLPLMEGL 661
DB 623 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPDRDSGLYDSSVPSSELSLPLMEGL 682
QY 662 STDQETSSLTSSVSSSGLEGEPPALPSKLLSGSCADLGCRTSYTDELHAVAP 717
DB 683 STDQETSSLTSSVSSSGLEGEPPALPSKLLSGSCADLGCRTSYTDELHAVAP 738

RESULT 10
AAU09957
ID AAU09957 standard; protein; 738 AA.

XX AC AAU09957;

XX DT 14-FEB-2002 (first entry)

XX DE Human Interleukin 17 (hIL-17) receptor like protein substitution #7.

XX KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
muten.

XX KW Homo sapiens.

OS OS Synthetic.

XX FT Key Location/Qualifiers

XX FT Misc-difference 602

XX FT /label= Cys, Ala, Ser

XX PN WO200168859-A2.

PD 20-SEP-2001.
XX 15-MAR-2001; 2001WO-US008678.
XX 16-MAR-2000; 2000US-0189816P.
PR 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX Jing S;
XX WPI; 2001-611392/70.
DR Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX Claim 24; Page; 158pp; English.
XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
XX osteopathic, vascular, cytostatic, anti-leukaemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone disease (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity. Note: This sequence is not given in the
XX specification but is based on the human Interleukin 17 (IL-17) receptor
XX like protein sequence (AAU09904) and has been created according to
XX information given in claim 24
XX SQ Sequence 738 AA;

Query Match 97.0%; Score 3714; DB 4; Length 738;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;

QY 2 DTCGWRKAAAPRLCVANEGVGPASRNSGLYNTFFKYDNCNTTYLNPVGKHVIAQAQMIT 61
DB 37 DTCGWR-----GVPASRNSGLYNTFFKYDNCNTTYLNPVGKHVIAQAQMIT 82
QY 62 ISOVACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCOQLILKDPKQLNSSFKR 121
DB 83 ISOVACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCOQLILKDPKQLNSSFKR 142
QY 122 TGMESQPFLLNKKFTDYFKVVPFSPISKNESNYHPFFRTRACDILLIOPNLACKPFWKP 181
DB 143 TGMESQPFLLNKKFTDYFKVVPFSPISKNESNYHPFFRTRACDILLIOPNLACKPFWKP 202
QY 182 RNLNISQHGSDMOVSFOHAPHNFGFRFFYLHYKLKHEGPPKRTCKOQTETTSCLLQN 241
DB 203 RNLNISQHGSDMOVSFOHAPHNFGFRFFYLHYKLKHEGPPKRTCKOQTETTSCLLQN 262
QY 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 301

Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
Qy 302 KKOENIYSHLDDESSSTVTAALPRERLRPRKVFCLYSSKDGQNHMNVQCFAYFLQ 361
Db 323 KKOENIYSHLDDESSSTVTAALPRERLRPRKVFCLYSSKDGQNHMNVQCFAYFLQ 382
Qy 362 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGEFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 481
Db 443 GSGKGEFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 502
Qy 482 NLPOLCSHLHSDHGLQEPGQHTQGSRRNYFRSKSGRSLYVAICNWHQFTDESPDWFEK 541
Db 503 NLPOLCSHLHSDHGLQEPGQHTQGSRRNYFRSKSGRSLYVAICNWHQFTDESPDWFEK 562
Qy 542 QFVFPFPPPLRYRFPVLEKFDGLVNDVMCKPGPESDFCLKVBAALVGLGATGPADSOHES 601
Db 563 QFVFPFPPPLRYRFPVLEKFDGLVNDVMCKPGPESDFCLKVBAALVGLGATGPADSOHES 622
Qy 602 QHGLDQDGEARPALDGSAAALQPLLHTVKAGSPSDMPRDSGYDSSVPSSELSLPLMEGL 661
Db 623 QHGLDQDGEARPALDGSAAALQPLLHTVKAGSPSDMPRDSGYDSSVPSSELSLPLMEGL 682
Qy 662 STDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAVAP 717
Db 683 STDQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDELHAVAP 738

RESULT 11

AAU09955
ID AAU09955 standard; protein; 738 AA.
XX AC AAU09955;
XX AC
XX AC
DT 14-FEB-2002 (first entry)
DE Human Interleukin 17 (hIL-17) receptor like protein substitution #5.
XX DE
XX DE
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cycostatic; anti-leukaemic; anti-infertility; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 385
FT /label= Cys, Ser, Ala
XX
XX WO200168859-A2.
PN 20-SEP-2001.
XX
XX 15-MAR-2001; 2001WO-US008678.
XX
XX 16-MAR-2000; 2000US-0189816P.
PR 28-NOV-2000; 2000US-0072460.
XX
XX (AMGE-) AMGEN INC.
XX
XX Jing S;
XX WPI; 2001-611392/70.
XX
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful

PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes, psoriasis and glaucoma.
XX
XX Claim 22; Page; 158pp; English.
XX
XX The invention describes novel nucleic acids encoding interleukin (IL) 17 receptor like polypeptides useful as vaccines and in gene therapy. These have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial, immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal, anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological, osteopathic, vascular, cycostatic, anti-leukaemic, anti-infertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. Note: This sequence is not given in the specification but is based on the human Interleukin 17 (IL-17) receptor like protein sequence (AAU09904) and has been created according to information given in claim 22

Sequence 738 AA;

Query Match 97.0%; Score 3714; DB 4; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 699; Conservative 1; Mismatches 2; Indels 14; Gaps 1;
Qy 2 DTCGRMKAARPLRCVANEVGPASRNSGLYNITFKYDNCCTTYLNPVGRHVIADAQNIT 61
Db 37 DTCGWR-----GVGPASRNSGLYNITFKYDNCCTTYLNPVGRHVIADAQNIT 82
Qy 62 ISOYACHDQVAVTILNSPGALGIEFLKGFVILEELKSEGRQCOQLILKDPKQLNSFKR 121
Db 83 ISOYACHDQVAVTILNSPGALGIEFLKGFVILEELKSEGRQCOQLILKDPKQLNSFKR 142
Qy 122 TGMESQPLNMKFETDYFVKVVPFPSPISKNSNYHPFFRTRACDLLLPDNLACKPFWKP 181
Db 143 TGMESQPLNMKFETDYFVKVVPFPSPISKNSNYHPFFRTRACDLLLPDNLACKPFWKP 202
Qy 182 RNLNISQHGSDMQVSPDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTTFSTCLQN 241
Db 203 RNLNISQHGSDMQVSPDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTTFSTCLQN 262
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 301
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAMAITVPLVVISAFATLFTVMCR 322
Qy 302 KKOENIYSHLDDESSSTVTAALPRERLRPRKVFCLYSSKDGQNHMNVQCFAYFLQ 361
Db 323 KKOENIYSHLDDESSSTVTAALPRERLRPRKVFCLYSSKDGQNHMNVQCFAYFLQ 382
Qy 362 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGEFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 481
Db 443 GSGKGEFLVAVSAIAEKLRQAKOSSAALSCKFTAVTFDYSCGDVPGILDLSKYRLMD 502

Qy 482 NLPQCSHLHSDHGLQPGQHTQGSRRNYFRSKSGSLYVAICNMHQFIDEPPDWFEK 541
Db 503 NLPQCSHLHSDHGLQPGQHTQGSRRNYFRSKSGSLYVAICNMHQFIDEPPDWFEK 562
Qy 542 QFVFPHPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGATGPADSQHES 601
Db 563 QFVFPHPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAPVLGATGPADSQHES 622
Qy 602 QHGGLDQGEARPALDQSAALQPLHTTVKAGSPDMPDRDGIYDSSVPSSLSLPLMEGL 661
Db 623 QHGGLDQGEARPALDQSAALQPLHTTVKAGSPDMPDRDGIYDSSVPSSLSLPLMEGL 682
Qy 662 STDQTSSLTSSVSSSSGLGEEPPALPSPKLLSSGCKADLGCRSYTDELHAPV 717
Db 683 STDQTSSLTSSVSSSSGLGEEPPALPSPKLLSSGCKADLGCRSYTDELHAPV 738

RESULT 12

ID ADB65245
ADB65245 standard; protein; 728 AA.

XX AC ADB65245;

XX DT 04-DEC-2003 (first entry)

XX DE Human protein encoded by clone TESTI20046540.

XX KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.

XX OS Homo sapiens.

XX PN EP1308459-A2.

XX PD 07-MAY-2003.

XX PF 28-MAR-2002; 2002EP-00007401.

XX PR 05-NOV-2001; 2001JP-00379298.

XX PR 25-JAN-2002; 2002US-00350978.

XX PA (HELI-) HELIX RES INST.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WIPI; 2003-450961/43.

XX DR N-PSDB; ADB63275.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
XX marker or medicines for regulation of their expression and activity, or
XX as targets of gene therapy.

XX PS Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
XX from 1970 fully defined nucleotide sequences which encode novel
XX polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
XX or its partial peptide, an antibody binding to the polypeptide or peptide
XX of the polynucleotide, immunologically assaying the polypeptide or
XX peptide of the polynucleotide by contacting the polypeptide or peptide
XX with the antibody of the encoded protein, and observing the binding
XX between the two, a transformant carrying the polynucleotide in an
XX expressible manner and an antisense polynucleotide. The oligonucleotide
XX is useful as a primer for synthesising the polynucleotide, or as a probe
XX for detecting the polynucleotide. The polynucleotides and encoded
XX proteins are useful as pharmaceutical agents and many disease-related
XX genes may be included in them, for developing a diagnostic marker or
XX medicines for regulation of their expression and activity, or as targets

CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.

XX Sequence 728 AA;

Qy Query Match 96.8%; Score 3708; DB 7; Length 728;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 21 EGVGPASRNSGLYNTFKYDNCCTTYLNPVGVKHVITADQAQNTISQYACHDQVAVTILWSPG 80
Db 31 QGVGPASRNSGLYNTFKYDNCCTTYLNPVGVKHVITADQAQNTISQYACHDQVAVTILWSPG 90
Qy 81 ALGIEFLKGRPVILEELKSEGRQCOQLILKDPKOLNSSFKRTGMESQPFLLNMKFTDYFV 140
Db 91 ALGIEFLKGRPVILEELKSEGRQCOQLILKDPKOLNSSFKRTGMESQPFLLNMKFTDYFV 150
Qy 141 KVPFPFSIKNESNYHPPFFRTRACDLLLLQPDNLACKPFWKPRNLNISQHSMDQVSPDHA 200
Db 151 KVPFPFSIKNESNYHPPFFRTRACDLLLLQPDNLACKPFWKPRNLNISQHSMDQVSPDHA 210
Qy 201 PHNFGFRFFYLHYKLKHEGPPFKRTKQEQOTTETSCLLQNVSPGDYIIELVDDNTTTRK 260
Db 211 PHNFGFRFFYLHYKLKHEGPPFKRTKQEQOTTETSCLLQNVSPGDYIIELVDDNTTTRK 270
Qy 261 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQOENYSHLDESSSS 320
Db 271 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQOENYSHLDESSSS 330
Qy 321 TYTAALPRERLRPRPKVFLCYSSKDGQNMNVQCFAYFLQDFCCEVALDLWEDFSLCR 380
Db 331 TYTAALPRERLRPRPKVFLCYSSKDGQNMNVQCFAYFLQDFCCEVALDLWEDFSLCR 390
Qy 381 EGQREWVIQTHESQFIIVVCSKGMKYFVDKKNYKHGSGRGSGELFLVAVSAIAEKL 440
Db 391 EGQREWVIQTHESQFIIVVCSKGMKYFVDKKNYKHGSGRGSGELFLVAVSAIAEKL 450
Qy 441 ROAQSSAALSRTAVYFDYSCGDVPGIILDSTKYRLMDNLPCSCHLHSDHGLQBP 500
Db 451 ROAQSSAALSRTAVYFDYSCGDVPGIILDSTKYRLMDNLPCSCHLHSDHGLQBP 510
Qy 501 QOHTROGSRNNYFRSKSGSLYVAICNMHQFIDEPPDWFEKQFVFPHPPLRYREPVLK 560
Db 511 QOHTROGSRNNYFRSKSGSLYVAICNMHQFIDEPPDWFEKQFVFPHPPLRYREPVLK 570
Qy 561 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQGEARPALDQSA 620
Db 571 FDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQGEARPALDQSA 630
Qy 621 ALQPLHTTVKAGSPDMPDRDGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSVSSSSG 680
Db 631 ALQPLHTTVKAGSPDMPDRDGIYDSSVPSSLSLPLMEGLSTDQTTSSLTSSVSSSSG 690
Qy 681 LGEHEPPALPSKLLSSGCKADLGCRSYTDELHAPV 718
Db 691 LGEHEPPALPSKLLSSGCKADLGCRSYTDELHAPV 728

RESULT 13

ID AAU04958
AAU04958 standard; protein; 728 AA.

XX AC AAU04958;

XX DT 24-OCT-2001 (first entry)

Db 423 NYKHGGGSGKGEFLVAVSAIAEKLRAQAKSSAALSXFIAYFYDSCGDPVPGILD 482
 Qy 473 LSTKYRLMDNLPQLCSHLHSDHGLQEPQOHTROGSRNRYFRSKGSLYVAICNMHQFI 532
 Db 483 LSTKYRLMDNLPQLCSHLHSDHGLQEPQOHTROGSRNRYFRSKGSLYVAICNMHQFI 542
 Qy 533 DEEDWFEKQVFPFHPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 592
 Db 543 DEEDWFEKQVFPFHPPLRYREPVLKFDGSLVNDVMCKPGPESDFCLKVEAAVLGAT 602
 Qy 593 GPADSOHSGGGLDQDGEARPAIDGSAALPILHTYKAGSPDMPRDSGYDSSVPSSE 652
 Db 603 GPADSOHSGGGLDQDGEARPAIDGSAALPILHTYKAGSPDMPRDSGYDSSVPSSE 662
 Qy 653 LSLPLMEGLSDQTETSSLTSSVSSSGLGEEPPALPSKLLSGSGCKADLGCRSYTDEL 712
 Db 663 LSLPLMEGLSDQTETSSLTSSVSSSGLGEEPPALPSKLLSGSGCKADLGCRSYTDEL 722
 Qy 713 HAVAPL 718
 Db 723 HAVAPL 728

RESULT 14
 ABU89705
 ID ABU89705 standard; protein; 728 AA.
 AC ABU89705;
 XX
 DT 10-JUL-2003 (first entry)
 XX
 DE Human interleukin 17 homologue PRO20026.
 XX
 KW Human; interleukin 17; IL-17; IL17 receptor; angiogenesis;
 KW T-lymphocyte proliferation; inflammatory cell infiltration;
 KW immune related disorder; systemic lupus erythematosus; osteoarthritis;
 KW rheumatoid arthritis; spondyloarthritis; systemic sclerosis;
 KW Sjogren's syndrome; sarcoidosis; autoimmune haemolytic anaemia;
 KW thyroiditis; diabetes mellitus; immune-mediated renal disease;
 KW demyelinating disease; Guillain-Barre syndrome; hepatobiliary disease;
 KW hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis;
 KW immune-mediated skin disease; erythema multiforme; contact dermatitis;
 KW allergic disease; asthma; atopic dermatitis; food hypersensitivity;
 KW urticaria; immunologic disease of the lung; eosinophilic pneumonia;
 KW idiopathic pulmonary fibrosis; transplantation associated disease;
 KW graft-versus-host disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003003546-A1.
 XX
 PD 02-JAN-2003.
 XX
 PF 22-MAR-2001; 2001US-00816744.
 XX
 PR 15-MAY-1998; 98US-0085579P.
 PR 23-DEC-1998; 98US-0113621P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 21-APR-1999; 99US-0130232P.
 PR 26-APR-1999; 99US-0130222P.
 PR 14-MAY-1999; 99US-0031183Z.
 PR 14-MAY-1999; 99US-0134287P.
 PR 14-MAY-1999; 99WO-US010733.
 PR 09-JUN-1999; 99US-0138387P.
 PR 23-DEC-1999; 99US-0172096P.
 PR 30-DEC-1999; 99WO-US031274.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 02-JUN-2000; 2000WO-US015264.

PR 22-JUN-2000; 2000US-0213807P.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 24-OCT-2000; 2000US-0242837P.
 PR 26-OCT-2000; 2000US-0244072P.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032878.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 XX (GETH) GENENTECH INC.
 XX
 PI Chen J, Filvaroff E, Fong S, Coddard A, Godowski P, Grimaldi C;
 PI Gurney A, Li H, Hillan K, Tumas D, Vanlookeren M, Vandien R;
 PI Watanabe C, Williams PM, Wood WI, Yansura D;
 XX
 DR MPI; 2003-428843/40.
 DR N-FSDB; ACA89858.
 XX
 XX New PRO polypeptides and polynucleotides homologous to interleukin-17,
 PT useful for treating e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, or systemic
 PT sclerosis.
 XX
 PS Claim 10; Fig 18; 129pp; English.
 XX
 CC The invention relates to a nucleic acid having similarity to interleukin-
 CC 17 (IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence
 CC identity to a nucleotide sequence which: (a) encodes a polypeptide having
 CC a sequence of appearing as ABU89697-ABU89700 and ABU89702-ABU89705 (PI-
 CC p8), lacking or having its associated signal peptide; (b) encodes an
 CC extracellular domain of PI-p8 lacking its associated signal peptide; (c)
 CC consists of a sequence of appearing as ACA89850-ACA89853 and ACA89855-
 CC ACA8985867; or (d) consists of the full-length coding sequence of
 CC selected from SI-S8, and of the cDNA deposited under ATCC accession
 CC number 209866, 203522, PTA-1185, PTA-2108, PTA-202, PTA-1535, PTA-1082 or
 CC PTA-2591. Also included are expression vectors, host cells, encoded
 CC proteins, chimaeric proteins, antibodies, ant/agonists, compounds
 CC inhibiting the expression of SI-S8 or activity (or mimicking the activity
 CC of) of PI-p8, stimulating/inhibiting the proliferation of T-lymphocytes
 CC using the polypeptides or ant/agonists, enhancing the infiltration of
 CC inflammatory cells into a tissue of a mammal by administering a PRO1031
 CC polypeptide, its an agonist or antagonist, and inhibiting angiogenesis
 CC induced by a PRO1031 polypeptide or its agonist in a mammal by
 CC administering a PRO1031 polypeptide, its ant/agonist or an anti-PRO1031
 CC antibody. The proteins, antibodies, ant/agonists and compounds are useful
 CC for treating an immune related disorder such as systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, a spondyloarthritis, systemic sclerosis, an idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
 CC demyelinating disease of the central or peripheral nervous system, a
 CC idiopathic demyelinating polynuropathy, Guillain-Barre syndrome, a
 CC chronic inflammatory demyelinating polynuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents an IL17 or
 CC IL17 receptor homologue of the invention
 XX
 SQ Sequence 728 AA;

Query Match 96.7%; Score 3703; DB 6; Length 728;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

Search completed: August 9, 2005, 11:44:55
Job time : 119.169 secs

chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin disease, bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, immunologic disease of the lung, eosinophilic pneumonias, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, transplant-associated disease, graft rejection or graft-versus-host disease. The composition is useful in treating the above-mentioned immune-related diseases in a mammal, or in increasing or inhibiting the proliferation of T-lymphocytes, or increasing or decreasing the infiltration of inflammatory cells into a tissue of a mammal. The present sequence represents a PRO polypeptide of the invention

XX Sequence 728 AA;

Query Match 96.7%; Score 3703; DB 6; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

| | | | |
|----|-----|--|-----|
| QY | 7 | RKAAARPLCVANE-GVGPASRNSGLNITFKYDNCCTYLNPGKHVIADAQNITISQY | 65 |
| DB | 3 | RASAGVPALFVSGQGVPASRNSGLNITFKYDNCCTYLNPGKHVIADAQNITISQY | 62 |
| QY | 66 | ACHDOVATILWSPALGIEFLKGRVILELKSREGCOQOLILKDPKQLNSSPKRTGME | 125 |
| DB | 63 | ACHDOVATILWSPALGIEFLKGRVILELKSREGCOQOLILKDPKQLNSSPKRTGME | 122 |
| QY | 126 | SQPLNLMKFETDYFKVVPFPPSIKNESNYHPPFFETRACDILLQPDNLACKPFWKPRNLN | 185 |
| DB | 123 | SQPLNLMKFETDYFKVVPFPPSIKNESNYHPPFFETRACDILLQPDNLACKPFWKPRNLN | 182 |
| QY | 186 | ISQ-----HGSDMQVSPDHAPHGSDMQVSPDHAPHGFRFFLHYLKHGEPFKRTCKEQTT | 232 |
| DB | 183 | ISQHGSDMQVSPDHAPHGSDMQVSPDHAPHGFRFFLHYLKHGEPFKRTCKEQTT | 242 |
| QY | 233 | ETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF | 292 |
| DB | 243 | EMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF | 302 |
| QY | 293 | ATLFTVMCRKQOENIYSHLDESESESTYTAALPRRLRPRPKVFLCYSSKQGNHNV | 352 |
| DB | 303 | ATLFTVMCRKQOENIYSHLDESESESTYTAALPRRLRPRPKVFLCYSSKQGNHNV | 362 |
| QY | 353 | VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQIHESQFIIVVCSKGMKYFVDKK | 412 |
| DB | 363 | VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQIHESQFIIVVCSKGMKYFVDKK | 422 |
| QY | 413 | NYKHGGGRGSGKGBFLVAVSAIAEKLRQAKQSSAALSKEFIAYFYDSCGDPVPGILD | 472 |
| DB | 423 | NYKHGGGRGSGKGBFLVAVSAIAEKLRQAKQSSAALSKEFIAYFYDSCGDPVPGILD | 482 |
| QY | 473 | LSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGRSLYVAICNMHOFI | 532 |
| DB | 483 | LSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGRSLYVAICNMHOFI | 542 |
| QY | 533 | DEPDWFEKQFVPFPPPLRYREPVLKFDPSGLVLDNVMCKPESDFCLKVEAAVLGAT | 592 |
| DB | 543 | DEPDWFEKQFVPFPPPLRYREPVLKFDPSGLVLDNVMCKPESDFCLKVEAAVLGAT | 602 |
| QY | 593 | GPADSQHESQHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSE | 652 |
| DB | 603 | GPADSQHESQHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSE | 662 |
| QY | 653 | LSLPLMEGLSTDQTTSTESVSSSSGLGEEPPALPSKILSSGCKADLCGRSYTDEL | 712 |
| DB | 663 | LSLPLMEGLSTDQTTSTESVSSSSGLGEEPPALPSKILSSGCKADLCGRSYTDEL | 722 |
| QY | 713 | HAVAPL 718 | |
| DB | 723 | HAVAPL 728 | |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:38:07 ; Search time 29.2862 Seconds
(without alignments)
1830.146 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGWRKAAARPLCVAN.....CKADLGCRSYTELHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 3703 | 96.7 | 728 | 4 | US-09-747-259-18 |
| 2 | 3703 | 96.7 | 728 | 4 | US-09-816-744-18 |
| 3 | 312 | 8.1 | 866 | 2 | US-08-620-694A-10 |
| 4 | 312 | 8.1 | 866 | 3 | US-09-022-255-10 |
| 5 | 312 | 8.1 | 866 | 3 | US-09-022-255-10 |
| 6 | 312 | 8.1 | 866 | 3 | US-08-978-773-4 |
| 7 | 312 | 8.1 | 866 | 3 | US-09-022-253-10 |
| 8 | 312 | 8.1 | 866 | 3 | US-09-022-260-10 |
| 9 | 312 | 8.1 | 866 | 3 | US-09-022-259-10 |
| 10 | 312 | 8.1 | 866 | 3 | US-09-022-257-10 |
| 11 | 312 | 8.1 | 866 | 4 | US-09-549-679-10 |
| 12 | 312 | 8.1 | 866 | 4 | US-10-033-522-1 |
| 13 | 306 | 8.0 | 864 | 2 | US-08-620-694A-2 |
| 14 | 306 | 8.0 | 864 | 3 | US-09-022-255-2 |
| 15 | 306 | 8.0 | 864 | 3 | US-09-022-696-2 |
| 16 | 306 | 8.0 | 864 | 3 | US-08-978-773-2 |
| 17 | 306 | 8.0 | 864 | 3 | US-09-022-253-2 |
| 18 | 306 | 8.0 | 864 | 3 | US-09-022-260-2 |
| 19 | 306 | 8.0 | 864 | 3 | US-09-022-259-2 |
| 20 | 306 | 8.0 | 864 | 3 | US-09-022-257-2 |
| 21 | 306 | 8.0 | 864 | 4 | US-09-549-679-2 |
| 22 | 135.5 | 3.5 | 385 | 4 | US-09-593-360B-106 |
| 23 | 135.5 | 3.5 | 502 | 4 | US-09-747-259-12 |
| 24 | 135.5 | 3.5 | 502 | 4 | US-09-816-744-12 |
| 25 | 135.5 | 3.5 | 504 | 4 | US-09-949-016-11658 |
| 26 | 116 | 3.0 | 552 | 4 | US-09-949-016-8005 |
| 27 | 113.5 | 3.0 | 617 | 3 | US-09-188-930-303 |

Sequence 303, App
Sequence 6384, Ap
Sequence 25826, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 9916, Ap
Sequence 9917, Ap
Sequence 10562, A
Sequence 14749, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 664, App
Sequence 6898, Ap

ALIGNMENTS

RESULT 1

US-09-747-259-18
; Sequence 18, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, F. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 18
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-18

Query Match 96.7%; Score 3703; DB 4; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

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QY 7 RMKAARPRLCVANE-CVGPSASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQY 65
DB 3 RASASGVPALFVSGEQGVGPASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQY 62

QY 66 ACHDOQAVTILWSPGALGIEFLKGFVRVILBELKSEGRQCQQLILKDPKQLNSPFRGTME 125
DB 63 ACHDOQAVTILWSPGALGIEFLKGFVRVILBELKSEGRQCQQLILKDPKQLNSPFRGTME 122

QY 126 SQPFLNMKFETDYFVKVVPFSPISKESNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 185
DB 123 SQPFLNMKFETDYFVKVVPFSPISKESNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 182

QY 186 ISO-----HGSDMQVSDHAPHNFGFRFFYLHYKLHKGFFKRTCKQBOQT 232
DB 183 ISOHGSDMQVSDHAPHNFGFRFFYLHYKLHKGFFKRTCKQBOQT 242

QY 233 ETTSCLLQNVSPGDIYIELVDNTTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 243 EMTSCLLQNVSPGDIYIELVDNTTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

QY 293 ATLTVMCRKKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKQGNMNV 352
DB 303 ATLTVMCRKKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKQGNMNV 362

QY 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIOKIHESQFIIVVCSKGMKYFVDKK 412
DB 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIOKIHESQFIIVVCSKGMKYFVDKK 422

QY 413 NYKHGGGRSGKGELFLVAVSAIAEKLROAKQSSAALSFKFIAYVPDYSCEGDVPGILD 472
DB 423 NYKHGGGRSGKGELFLVAVSAIAEKLROAKQSSAALSFKFIAYVPDYSCEGDVPGILD 482

QY 473 LSTKYRLMDNLPQLCSHLHSDHGLQBPQOHTROGSRNNYFRSKSGSLYVAICNMHQFI 532
DB 483 LSTKYRLMDNLPQLCSHLHSDHGLQBPQOHTROGSRNNYFRSKSGSLYVAICNMHQFI 542

QY 533 DEEPDWFEEKQVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 592
DB 543 DEEPDWFEEKQVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 602

QY 593 GPADSQHSQHGGLDQGEARPALDGSAAALQPLHTVKAGSPDMPRDSDGIYDSVPSSE 652
DB 603 GPADSQHSQHGGLDQGEARPALDGSAAALQPLHTVKAGSPDMPRDSDGIYDSVPSSE 662

QY 653 LSLPLMEGLSTDQETSTSLTESVSSSGLGEEPPALPSSKLLSSGCKADLGCRSYTDL 712
DB 663 LSLPLMEGLSTDQETSTSLTESVSSSGLGEEPPALPSSKLLSSGCKADLGCRSYTDL 722

QY 713 HAVAPL 718
DB 723 HAVAPL 728
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US-09-816-744-18
; Sequence 18, Application US/09816744
; Patent No. 6579520
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2 (US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; CURRENT FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 18
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-816-744-18

Query Match 96.7%; Score 3703; DB 4; Length 728;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

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QY 7 RMKAARPRLCVANE-CVGPSASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQY 65
DB 3 RASASGVPALFVSGEQGVGPASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQY 62

QY 66 ACHDOQAVTILWSPGALGIEFLKGFVRVILBELKSEGRQCQQLILKDPKQLNSPFRGTME 125
DB 63 ACHDOQAVTILWSPGALGIEFLKGFVRVILBELKSEGRQCQQLILKDPKQLNSPFRGTME 122

QY 126 SQPFLNMKFETDYFVKVVPFSPISKESNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 185
DB 123 SQPFLNMKFETDYFVKVVPFSPISKESNYHPFFRTRACDILLQPDNLACKPFWKPRNLN 182

QY 186 ISO-----HGSDMQVSDHAPHNFGFRFFYLHYKLHKGFFKRTCKQBOQT 232
DB 183 ISOHGSDMQVSDHAPHNFGFRFFYLHYKLHKGFFKRTCKQBOQT 242

QY 233 ETTSCLLQNVSPGDIYIELVDNTTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 243 EMTSCLLQNVSPGDIYIELVDNTTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

QY 293 ATLTVMCRKKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKQGNMNV 352
DB 303 ATLTVMCRKKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKQGNMNV 362

QY 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIOKIHESQFIIVVCSKGMKYFVDKK 412
DB 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIOKIHESQFIIVVCSKGMKYFVDKK 422

QY 413 NYKHGGGRSGKGELFLVAVSAIAEKLROAKQSSAALSFKFIAYVPDYSCEGDVPGILD 472
DB 423 NYKHGGGRSGKGELFLVAVSAIAEKLROAKQSSAALSFKFIAYVPDYSCEGDVPGILD 482

QY 473 LSTKYRLMDNLPQLCSHLHSDHGLQBPQOHTROGSRNNYFRSKSGSLYVAICNMHQFI 532
DB 483 LSTKYRLMDNLPQLCSHLHSDHGLQBPQOHTROGSRNNYFRSKSGSLYVAICNMHQFI 542

QY 533 DEEPDWFEEKQVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGAT 592
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| | | | |
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| Db | 543 | DEEPOWFEKQFVPPHPPLRYREPVELEKFDGLNDVMCKPSPDSDFCLKVEAAVLGAT | 602 |
| Qy | 593 | GPADSQHESQHCGGLQDGEARPALDGSAAALQPLIHTVKAGSPMDPRDSCGIYDSSVPSSE | 652 |
| Db | 603 | GPADSQHESQHCGGLQDGEARPALDGSAAALQPLIHTVKAGSPMDPRDSCGIYDSSVPSSE | 662 |
| Qy | 653 | LSIPLMEGLSTDTQTTSILTSVSSSSGLGEEPPALPSKLLSGSCKADLCGRSVTDEL | 712 |
| Db | 663 | LSIPLMEGLSTDTQTTSILTSVSSSSGLGEEPPALPSKLLSGSCKADLCGRSVTDEL | 722 |
| Qy | 713 | HAVAPL | 718 |
| Db | 723 | HAVAPL | 728 |

RESULT 3
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17

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Query Match      8.1%; Score 312; DB 2; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY      34 NITPKYDNC--TTVLNPPVGKHIADAQNIT-----ISQYACHDQ-----VAVTILWS 78
db      49 NCTVKNSTCLDSDSWTHP-----RNLTPSSPKDLQIQLHFAHTQGDLPFVAHIEWT 99

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| Qy | 79 | -PGALGIEFLKGRVILLEKSEGRQCOQLIKDPKOLNSSFKETGMESQOPLNKKFTD | 133 |
| Db | 100 | LQTDASLILYLEGAELSVLQNTNERLCV--FEFLSKLRHHHRWRFTFSHFV-VDPOQE | 156 |
| Qy | 138 | YFKVK--VPPFSIKNESNYHPFFRTRACDILLQPDNLACK---PFWKPRNL----- | 184 |
| Db | 157 | YEVTVHHLKPIDGDPNHQSKNPLVPDCEHARKMKTTPCMSGSLWDP-NITVETLEAH | 215 |
| Qy | 185 | -----NISQHSQDMQVSFDHAPNFGFRFFYLHYKLKHEGPFKREKTKCQBQTETT | 235 |
| Db | 216 | QLRVSFTLWNETHYQILLTSPFMENHSCFEHMH-HIPAPRBEFHORSNVTTLRLNKL | 274 |
| Qy | 236 | SCLLQNSPGDYIIEILDVDDT---NTTRKVMHYALKPVHSPWAGIPRAVAITVPLVVISAF | 292 |
| Db | 275 | GCCEHQVOIQPFSSCLNDCLRHSATVSCPEMPDTPPIPYMPLVWVWFITGISILLVG | 334 |
| Qy | 293 | ATLFTVMCRKKQENIYSHLDEESSESSTYTAALPREKLRRP---KVFLCYSSKDGQN | 348 |
| Db | 335 | SVILLIYCCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKPRKWIYISA-DHPL | 390 |
| Qy | 349 | HMNVOQCFAYFLQDFCCCEVALDLWEDFSLCREGQREWV---IQIHESOFIIVVCSKG | 404 |
| Db | 391 | YVDVVLKFAQFLLTACETEVALDLLEQAISEAGWMTVWGROKQEWESNSKIIIVLCNRG | 450 |
| Qy | 405 | MKYFVDYKXNYKHGGG-----RSGSGKGBELFLVAVSAIAEKLRQAKOSSAALSUKFTA | 456 |
| Db | 451 | TR---AKWQALLGRGAPVRLRCDHGKPKVGDLTAAAMNMLPDKR-----PACFGTVV | 501 |
| Qy | 457 | VYP-DYCEGDVPGIILDSLYKRLMDNLPLQCSHLHSHRDHGLQBQGHTRQG--SRNVYF | 513 |
| Db | 502 | CYSEVSCDGDVPLDFGAAPRYPLMDRFEV--YFRIODLEMFQGRMHRVGLSGDNYLV | 559 |
| Qy | 514 | RSKSGRLYVAICNMHQFIIDBEPDWFE-----KQFVPHPPPLRYREPVLKFXDSGL | 565 |
| Db | 560 | RSPCRQLRAALDRFRDQWVRCPDWFECENLYSADDQDAPSLDERV-FEPLLP-GTGI | 617 |
| Qy | 566 | VLNDVMCKPGPESFCFLKVEAAVLGATGPADSOHE-----SQHGG | 605 |
| Db | 618 | VKRAPLVRE-PGSQACLAIDLPLVGEEGAAVAKLEPHLQPRQPAPQLHTLVLAEEGA | 676 |
| Qy | 606 | LDQDGEARPALDGS---ALQ-----PLHTVVKAGSPDMPRDSGIVDSSVPSSLSLP | 656 |
| Db | 677 | LVAAVECPGLADGAANRLALAGEACPLIGSPGAG-----RNSVLP---LPVDPEDSP | 727 |
| Qy | 657 | LMEGLSTDQDTSTSLTESVSSSSGLGEBEPPALPSKILLSGSCKADLGC | 705 |
| Db | 728 | I--GSSTPMASPDILPEDVR-----EHLEGIMLSLPEOSLSCOAQGGC | 768 |

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RESULT 4
US-09-022-255-10
; Sequence 10, Application US/0902255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Farniow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255

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185 QY -----NISOHSDMOVSDHAPHNFGFRFFYLHYKLKHEGPFKRKCKEQOTTETT 235
216 Db QLRVSTFWNSTHYQIILTSFPHMNSCEHMH-HIPAPRPEEFHORSNVTLTLNLK 274
236 QY SCLQNVSPGYIIBLVDT---NTRKVMHYALKVHSPWAGPIRAVAITVPLVVISAF 292
275 Db GCRHQVQIQPFSSCLNCLRHSAVSCEPMPDTPPIPYMPLWYWFITGISILLVG 334
293 QY ATLFTVMCRKQOENIYSHLDESESTYTAALPRERLRPP-----KVFLCYSKQOQN 348
335 Db SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKRKVMYIISA-DHPL 390
349 QY HNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREW---IQKHESQFIIVVCSKG 404
391 Db YDVVVLKFAQFLITACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
405 QY MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLRQAQKSSAALSKEFIA 456
451 Db TR-----AKQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYV 501
457 QY VYF-DYSCGDPVPGILDSTKYRLMDNLPOLCSHLHSDHGLQBPQHTROG--SRRNYF 513
502 Db CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQGRMHRVGEISGDNYL 559
514 QY BSKGRSLYVAICNMHQIIDEEDWFE-----KQFVPPHPPPLRYREPVLKFDGSL 565
560 Db RSPGGRQLRAALDRFRDQVRCDFWECENYSADDQDAPSLDERV-FEELPLPP-GTGI 617
566 QY VLNDVMCKPGPSDFCLKVEAAVLGATGPADSQHE-----SQRGG 605
618 Db VKRAPLVRE-PSQAQCLAIPLVGEAGAAVAKLEPHLQPRQAPQPLHTLVLAEEGA 676
606 QY LDQGEARPALDGA---ALQ-----PLLHTVKAGSPDMPRDSGIVDSSVPSSELSLP 656
677 Db LVAAVEPGPLADGAARLALAGEGACPLLGSPGAG-----RNSVLF--LPVDPEDSP 727
657 QY LMEGLSTDOTETSSLTESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
728 Db L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGGC 768

RESULT 6

US-08-978-773-4
; Sequence 4, Application US/08978773
; Patent No. 6083906
; GENERAL INFORMATION:
; APPLICANT: Troutt, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/978, 773
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/052,525
; FILING DATE: 27 NOVEMBER 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-4

Query Match 8.1%; Score 312; DB 3; Length 866;

Best Local Similarity 23.1%; Pred. No. 1.46-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 34 NITKYDNC--TTLNVPKGVIAADONIT-----ISQYACHDO-----VAVTILWS 78
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDIQIQLHFAHTQOGDLFPVAHIEWT 99
QY 79 -PGALGIEFLKGRFVILEELKSEGRQOQILKDPKQNSFSFKRTGMSQPLNMKFTD 137
Db 100 LOTDASILYLEGALSVLQNTNEELCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDQE 156
QY 138 YFVKV--VPPFSIKNSYHPFPRTRACDILLQPDNLAK---PFWKPRNL-----184
Db 157 YEVTVHLKPIPDGDPNHQSKNLPDPCHEARMKVTTPCMSSGSLMDP-NITVETLEAH 215
QY 185 -----NISOHSDMOVSDHAPHNFGFRFFYLHYKLKHEGPFKRKCKEQOTTETT 235
Db 216 QLRVSTFWNSTHYQIILTSFPHMNSCEHMH-HIPAPRPEEFHORSNVTLTLNLK 274
QY 236 SCLQNVSPGYIIBLVDT---NTRKVMHYALKVHSPWAGPIRAVAITVPLVVISAF 292
Db 275 GCRHQVQIQPFSSCLNCLRHSAVSCEPMPDTPPIPYMPLWYWFITGISILLVG 334
QY 293 ATLFTVMCRKQOENIYSHLDESESTYTAALPRERLRPP-----KVFLCYSKQOQN 348
Db 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKRKVMYIISA-DHPL 390
QY 349 HNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREW---IQKHESQFIIVVCSKG 404
Db 391 YDVVVLKFAQFLITACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCSRG 450
QY 405 MKYFVDKKNYKHGGG-----RSGKGELFLVAVSAIAEKLRQAQKSSAALSKEFIA 456
Db 451 TR-----AKQALLGRGAPVRLRCDHGKPVGDLFTAAMNMILPDFKR-----PACFGTYV 501
QY 457 VYF-DYSCGDPVPGILDSTKYRLMDNLPOLCSHLHSDHGLQBPQHTROG--SRRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQGRMHRVGEISGDNYL 559
QY 514 BSKGRSLYVAICNMHQIIDEEDWFE-----KQFVPPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQLRAALDRFRDQVRCDFWECENYSADDQDAPSLDERV-FEELPLPP-GTGI 617
QY 566 VLNDVMCKPGPSDFCLKVEAAVLGATGPADSQHE-----SQRGG 605
Db 618 VKRAPLVRE-PSQAQCLAIPLVGEAGAAVAKLEPHLQPRQAPQPLHTLVLAEEGA 676
QY 606 LDQGEARPALDGA---ALQ-----PLLHTVKAGSPDMPRDSGIVDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARLALAGEGACPLLGSPGAG-----RNSVLF--LPVDPEDSP 727
QY 657 LMEGLSTDOTETSSLTESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGGC 768

RESULT 7

US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305

SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-260-10

Query Match 8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 34 NITKYDNC--TTLNVPVKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 78
DB 49 NCTVKNSTCLDDSWHP-----RNLTPSSPKDLQIQLHFAHTQGGDLFPVAHIEWT 99
QY 79 -PGALGIEFLKGFVLEELKSEGRQCOQLILKDPKQLNSSFKTGMESQPLNKKFTD 137
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDQE 156
QY 138 YFVKV--VPFSPKSNESNYHPFFRTRACDLLLLQPDNLACK---PFWKPRNL-----184
DB 157 YEVTVHLLPKIPDGDPNHQSKNFLVPDCEHARMKVTPPCMSGSLMDP-NITVETLEAH 215
QY 185 -----NISQHSMDQVSDFHAPHNFGFRFFLYLHYKLHKGFPFKKTKCKQQTETT 235
DB 216 QLRVSFTLWNESTHYQILLTSFPMENHSCFEHMH-HIPAPRPEFHQSRNVTLTLRLNK 274
QY 236 SCLLQNVSPGYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRHOVQIQPFSSCLNCLDRHSATVSCPMPDTPPEIPDYMPLVWYVFTGSIILVG 334
QY 293 ATLFTVMCRKQOENIYSHLDESESESTYTAALPRELRPRP-----KVFLCYSSKQGN 348
DB 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKPRKWIYISA-DHPL 390
QY 349 HNVVQCFAFYLDQFCGCEVALDLWEDFSLCREGREW----IQKHESQFIIVVCSKG 404
DB 391 YDVLVKFAQFLLTACGTVEALDLLEEQAISEAGVWTVGKQKQEMVESNKIIIVLCRSG 450
QY 405 MKYFVDKKNYKHGGG-----RSGKGBELFLVAVSAIAEKLRQAKQSSAALSKEFIA 456
DB 451 TR-----AKWQALLGRGAPVRLRCDHGKVPVGDIFTAAMNMLPDKR-----PACFGTYV 501
QY 457 VYF-DYSCGDPVPGILDSTKRYLMDNLPLCASHLHSDHGLQEPQHTROG---SRRNYF 513
DB 502 CYFEVSCDGVDPDLFGAAPRPLMDRFEV--YFRIQDLEMFQGRHVRGELSGDNYL 559
QY 514 RSKGRSLYVAICNNHQFIDEPDWE-----KQFVFPHPPLRYREPVLEKFDGL 565
DB 560 RSPGGRQLRAALDRFDQVRCDFWECENLYSADDQADAPSIDDEV-FEELPLPP-GTGI 617
QY 566 VLNDVMCKGPBSPCLKVEAAVLGATGAPDSQHE-----SQHGG 605
DB 618 VKRAPLVRE-PGSOACLAIDPLVGBEGGAATAKLEPHLQPRGPAPQPLHTLVLAEEGA 676
QY 606 LDQGEARALDGA---ALQ-----PLLHTVKAQSPDPRDSIGYDSSVPSSELSLP 656
DB 677 LVAAVEPGLADGAARLALAGEACPLLGSPGAG-----RNSVLF--LPVDPDPS 727
QY 657 LMEGLSTDTQTTSTLATESVSSSGLGEBEPALPKLLSSGCKADLGC 705
DB 728 L---GSTPMASPDLLPEDVR-----EHLGLMLSLFEQSLSCQAQGGC 768

RESULT 9

US-09-022-259-10
Sequence 10, Application US/09022259
Patent No. 6191104
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-259-10

Query Match 8.1%; Score 312; DB 3; Length 866;

Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;

QY 34 NITKYDNC--TTLNVPVKHVIADAQNIT-----ISQYACHDQ-----VAVTILWS 78
DB 49 NCTVKNSTCLDDSWHP-----RNLTPSSPKDLQIQLHFAHTQGGDLFPVAHIEWT 99
QY 79 -PGALGIEFLKGFVLEELKSEGRQCOQLILKDPKQLNSSFKTGMESQPLNKKFTD 137
DB 100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDQE 156
QY 138 YFVKV--VPFSPKSNESNYHPFFRTRACDLLLLQPDNLACK---PFWKPRNL-----184
DB 157 YEVTVHLLPKIPDGDPNHQSKNFLVPDCEHARMKVTPPCMSGSLMDP-NITVETLEAH 215
QY 185 -----NISQHSMDQVSDFHAPHNFGFRFFLYLHYKLHKGFPFKKTKCKQQTETT 235
DB 216 QLRVSFTLWNESTHYQILLTSFPMENHSCFEHMH-HIPAPRPEFHQSRNVTLTLRLNK 274
QY 236 SCLLQNVSPGYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRHOVQIQPFSSCLNCLDRHSATVSCPMPDTPPEIPDYMPLVWYVFTGSIILVG 334
QY 293 ATLFTVMCRKQOENIYSHLDESESESTYTAALPRELRPRP-----KVFLCYSSKQGN 348
DB 335 SVILLIVCMWRLAGPGS---EKYSDDTKYTDGLPAADLIPLPKPRKWIYISA-DHPL 390
QY 349 HNVVQCFAFYLDQFCGCEVALDLWEDFSLCREGREW----IQKHESQFIIVVCSKG 404
DB 391 YDVLVKFAQFLLTACGTVEALDLLEEQAISEAGVWTVGKQKQEMVESNKIIIVLCRSG 450
QY 405 MKYFVDKKNYKHGGG-----RSGKGBELFLVAVSAIAEKLRQAKQSSAALSKEFIA 456

Db 451 TR-----AKWQALLGKGAFLRCDHGKVPGLDFTAAWMLLPDFKR-----PACFGTYV 501
Qy 457 VYF-DYCEGDPVGLDSTKYLMDNLPOICSHLHSDHGLQBPQHTROG--SRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 514 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQJRAALDRFRDQVRCDFWECENLYSADDQDAPSLDEEV-FEPLLP-GTGI 617
Qy 566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----SQHGG 605
Db 618 VKRAPLVRE-PSQAQCLAIIDLPGVEEGAAVAKLEPHLQPRGQAPAPQPLHLVLAABEGA 676
Qy 606 LDQDGEARPALDGA---ALQ-----PLHTVKGSPSDMPRDSGIYDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARVLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 657 LMEGLSTDTQETSSLTESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 10

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-257-10

Query Match 8.1%; Score 312; DB 3; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
Qy 34 NITPKYDNC--TYYLNPVGHVIAQAQNT-----ISOYACHDQ-----VAVTILMS 78
Db 49 NCTVKNSTCLDDSWIHP-----RNLTPSSPKDQLQIHLFAHTQQDGLFPVAHIEWT 99
Qy 79 -PGALGTEFLKGRVILLEELKSEGRQCOQLLLDKPKOLNSSFKTKTGMESQPELNMKMETD 137
Db 100 LQTDASLYLEGAELSVLQNTNTERLCVR--FRLSKLRHHRRWRFTFHFV-VDPDQE 156
Qy 138 YFVKV--VPPFSIKNESNYHPFFRTRACDILLQPDMLACK---PFWKPRNL----- 184
Db 157 YEVTVHLKPIPDGDPNHQSKNPLVPDCEHARKVTTTPCMSSGSLWDP-NITVETLEAH 215
Qy 185 -----NISQHSMDQVSDHAPHNFRFRFYLYHLKHEGFPKRCKTKQBQQTETT 235
Db 216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRDEEFPHQSNVLTILNLK 274
Qy 236 SCLLQNVSPGDYIIELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAF 292
Db 275 GCCRHQVQIQIPFFSSCLNCLRHSATVSCPEMPDTPPEIPDYMWPLYWYFITGISILVG 334
Qy 293 ATLFTVMCRKKQDENIYSHLDESSSESTYTAALPRERLRPRP----KVFCLYSSKDGQN 348
Db 335 SVILLIIVMTWRLAGPGS---EKYSDTKYTDGLPAADLPPPLKPRKWIILYSA-DHPL 390
Qy 349 HMNVOCFAYFLQDFCGCEVALDLMEDFSLCREGQREW---IQKTHESQFIIVVCSKG 404
Db 391 YVDVVLKFAQFLLTACGTEVALDLLEQAISEAGVMTWVGKQKQEMVESNKIIVLCRSG 450
Qy 405 MKYFVDKKNYKHGGG-----RSGKGELFLVAISAIAEKLRQAKQSSAALSFKFIA 456
Db 451 TR-----AKWQALLGKGAFLRCDHGKVPGLDFTAAWMLLPDFKR-----PACFGTYV 501
Qy 457 VYF-DYCEGDPVGLDSTKYLMDNLPOICSHLHSDHGLQBPQHTROG--SRNYF 513
Db 502 CYFSEVSCDGVDPDLFGAAPRYPLMDRPEEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 514 RSKGRSLYVAICNMHQFIDEEPWFE-----KQVPHPPPLRYREPVLKFDGSL 565
Db 560 RSPGGRQJRAALDRFRDQVRCDFWECENLYSADDQDAPSLDEEV-FEPLLP-GTGI 617
Qy 566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----SQHGG 605
Db 618 VKRAPLVRE-PSQAQCLAIIDLPGVEEGAAVAKLEPHLQPRGQAPAPQPLHLVLAABEGA 676
Qy 606 LDQDGEARPALDGA---ALQ-----PLHTVKGSPSDMPRDSGIYDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARVLALAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 657 LMEGLSTDTQETSSLTESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768

RESULT 11

US-09-549-679-10
; Sequence 10, Application US/09549679
; Patent No. 6680057
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,679
FILING DATE: 14-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-549-679-10

Query Match 8.1%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 34 NITPKYDNC--TYYLNPVGHKVIADAQNIT-----ISOYACHDQ-----VAVTIILWS 78
DB 49 NCTVKNSTCLDDSWIHP-----RNLTSSPKDLQIQLHFAHTQQGDLFPVVAHIWNT 99
QY 79 -PGALGIEFLKGFVILBELKSEGRQCQQLILKDPKQLNSSFKRTGMSQPLNKKFTD 137
DB 100 LQTDASILYLEGAELSVLQANTNERLCVR--FEFLSKLRHHRRWRFTFSHFV--VDPDOE 156
QY 138 YFVKV--VPFPIKSNESYHPFFRTRACDILLQPDNLACK---PFWKPRNL-----184
DB 157 YEVTVHLLPKPIPDGDPNHQSKNFLVPDCEHARMKVITPCMSGSLMDP-NITVETLEAH 215
QY 185 -----NISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRKCTCKEQTTETT 235
DB 216 QLRVSFTLWNSTHYQILLTSPPHNHSCEFEMH-HIPAPRPEEFHORSNVTLLRNLK 274
QY 236 SCLLQNVSPGDYIIELVDDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRQVQIQPFSSCLNCLRHSAVSCPEMPDPEPIPDYMLVWYVFTIGSILLVG 334
QY 349 HNNVQCFCAYFLQDFCGCEVALDLWEDFSLCREQREW----IQIHESQFIIVVCSKG 404
DB 391 YVDVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWVGKQKQEMVESNSKIIVLCSRG 450
QY 405 MKYFVDKKNYKHKGKGG-----RGSGKGELFLVAVSAIAEKLRQAQSSAALSKFIA 456
DB 451 TR-----AKWQALLGRGAPVRLRCDKGKPVGDLFTAAMNMLPDKFR-----PACFGTYV 501
QY 457 VYF-DYSCGDPVGLDLSKYRLMDNLPQLCSHLHSDHGLQEPGQHTROG--SRNYV 513
DB 502 CYFSEVSCDGDVPDILFGAAPRPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
QY 514 RSKSGRLVAICNMHQFIDEFPDWE-----KQFVFPFPPPLRYREPVLKFDGSL 565

DB 560 RSPGGRQLRAALDRFRDQVRCPDWFECENLYSADDQDAPSLDEEV-FEELPLPP-GTGI 617
QY 566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHE-----SQHGG 605
DB 618 VKRAPLVRE-PSQACLAIDPLVGEEGA-AVAKLEPHLQPRGQPAQPLHTLVLAABEGA 676
QY 606 LDQGEARPALDGA---ALQ-----PLLHTVAGSPDMPDRSGIYDVSVPSELSLP 656
DB 677 LVAAVEPGPLADGA-AVRLALAGEGEACPLLGSPAG-----RNSVLP--LPVDPEDSP 727
QY 657 LMEGLSLDQTETSSLTESVSSSSSGEEREPALPSKLLSSSGCKADLGC 705
DB 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768
RESULT 12
US-10-033-522-1
; Sequence 1, Application US/10033522
; Patent No. 6793919
; GENERAL INFORMATION:
; APPLICANT: MOHLER, Kendall M.
; TITLE OF INVENTION: Methods for Treating Rheumatoid Arthritis Using IL-17 Antagonists
; FILE REFERENCE: 2982-A
; CURRENT APPLICATION NUMBER: US/10/033,522
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: US 60/241,230
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-522-1

Query Match 8.1%; Score 312; DB 4; Length 866;
Best Local Similarity 23.1%; Pred. No. 1.4e-23;
Matches 178; Conservative 107; Mismatches 338; Indels 146; Gaps 34;
QY 34 NITPKYDNC--TYYLNPVGHKVIADAQNIT-----ISOYACHDQ-----VAVTIILWS 78
DB 49 NCTVKNSTCLDDSWIHP-----RNLTSSPKDLQIQLHFAHTQQGDLFPVVAHIWNT 99
QY 79 -PGALGIEFLKGFVILBELKSEGRQCQQLILKDPKQLNSSFKRTGMSQPLNKKFTD 137
DB 100 LQTDASILYLEGAELSVLQANTNERLCVR--FEFLSKLRHHRRWRFTFSHFV--VDPDOE 156
QY 138 YFVKV--VPFPIKSNESYHPFFRTRACDILLQPDNLACK---PFWKPRNL-----184
DB 157 YEVTVHLLPKPIPDGDPNHQSKNFLVPDCEHARMKVITPCMSGSLMDP-NITVETLEAH 215
QY 185 -----NISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPFKRKCTCKEQTTETT 235
DB 216 QLRVSFTLWNSTHYQILLTSPPHNHSCEFEMH-HIPAPRPEEFHORSNVTLLRNLK 274
QY 236 SCLLQNVSPGDYIIELVDDT---NTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
DB 275 GCCRQVQIQPFSSCLNCLRHSAVSCPEMPDPEPIPDYMLVWYVFTIGSILLVG 334
QY 293 ATLFTVMCRKQKQENIYSHLDESESSSTYTAALPRERLRPR-----KVFLCYSSKDGON 348
DB 335 SVILLIVCMTWRLAGPGS---EKYSDDTKYTDGLPAADLIPPLKPRKWIYISA-DHPL 390
QY 349 HNNVQCFCAYFLQDFCGCEVALDLWEDFSLCREQREW----IQIHESQFIIVVCSKG 404
DB 391 YVDVVLKFAQLLTACGTEVALDLLEEQAISEAGVMTWVGKQKQEMVESNSKIIVLCSRG 450
QY 405 MKYFVDKKNYKHKGKGG-----RGSGKGELFLVAVSAIAEKLRQAQSSAALSKFIA 456
DB 451 TR-----AKWQALLGRGAPVRLRCDKGKPVGDLFTAAMNMLPDKFR-----PACFGTYV 501
QY 457 VYF-DYSCGDPVGLDLSKYRLMDNLPQLCSHLHSDHGLQEPGQHTROG--SRNYV 513

Db 502 CYFSEVSCDGDVDPDLFGAAPRYPLMDRFEV--YFRIQDLEMFQGRMHRVGLSGDNYL 559
Qy 514 RSKGRSLYVAICNMHQFIDEPDWE-----KQFVPHPPPLRYREPVLEKFSGL 565
Db 560 RSPGGRQLRAALDRFQWQRCPDWFECENIYSADDDQDAPSLDEEV-FEEPLPP-GTGI 617
Qy 566 VLNDVMCKPGESDFCLKVEAAVLGATGPADSOHE-----SOHGG 605
Db 618 VKRAPLVRE-PSQOCLAIDPLVGEEGA-AVAKLEPHLQPRGQAPQPLHTLVLAABEGA 676
Qy 606 LDQGEARPALDGS---ALQ-----PLLHTVXAGSPDMRPSGGIYDSSVPSSELSLP 656
Db 677 LVAAVEPGPLADGAARLALAGEAGEACPLLGSPGAG-----RNSVLF---LPVDPEDSP 727
Qy 657 LMEGLSTDQTTSTLSESVSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db 728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSQAQGGC 768

RESULT 13

US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620.694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-620-694A-2

Query Match 8.0%; Score 306; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 6.1e-23;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
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Qy 107 --LILKDPKOLNLSFKRTGMESQPFLLNMKFTEDYFVVKVPFPSPKIKNSNYHPFFRTRAC 164
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Qy 196 SFD-----HAPHNFGFRFFLYHKLKHE---GPFKRKTKCQQTITTCLL 239
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Db 342 IICMTWRLSGADQEKHGDDSKINGILPVAULTPPPLRPR-KWIVVISA-DHPLYVEVVLK 399
Qy 356 FAYFLQDFCCCEVALDLWEDFSLCREQOREWVQK-----IHESQFIIVVCSKGMKYFVDK 411
Db 400 FAQLITACTEVALDLLEEQVISEVGVMTWVRQKQEMVESNKIILCSR-----TQ 454
Qy 412 KNYKHGG-----GRGSGKGLFVAVSAIAEKROAKQSSAALS\$KFTAVIFYDY 461
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Qy 462 SC-EGDVPGLDLS\$TKYRLMDNLPLQCSHLH\$RDHGLQ\$EPQ--HTROGSRNRYFR\$KSG 518
Db 510 IC\$ERDVPDLFNIT\$RYPLMDRFEV--YFRIQDLEMFQGRMHRVREL\$TGDNYLQ\$PSG 567
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Qy 614 PALDGSAAQLPL\$HTV\$KAG\$PSDMP--RDS-----GIYD\$SV---P\$SEL\$SLP\$----- 657
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RESULT 14

US-09-022-255-2
; Sequence 2, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022.255
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/620,694
FILING DATE: 21 MARCH 1996
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 864 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-255-2

Query Match      8.0%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 6.1e-23;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;

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DB 17 GWLILLNLVAPGRSPRLDPAPVCAQEGSLSCVKNSTCLDDSWIHPKNLTSPSPKNI 76
QY 52 HVIADAQNTISQYACHDOAVT-ILMS-PGALGIEFLKGFVILEELKSEGRQCOQ--- 106
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; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-2

Query Match      8.0%; Score 306; DB 3; Length 864;
Best Local Similarity 22.5%; Pred. No. 6.1e-23;
Matches 189; Conservative 129; Mismatches 320; Indels 202; Gaps 42;
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GenCore version 5.1.6
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(without alignments)
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Title: US-10-717-282-1

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Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 10% summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2383 | 100.0 | 2383 | 18 US-10-717-282-1 | Sequence 1, Appli |
| 3 | 2376.6 | 99.7 | 2383 | 9 US-09-912-157-4 | Sequence 4, Appli |
| 4 | 2376.6 | 99.7 | 2383 | 18 US-10-717-282-4 | Sequence 4, Appli |
| 5 | 2289 | 96.1 | 2341 | 9 US-09-912-157-7 | Sequence 7, Appli |
| 6 | 2289 | 96.1 | 2341 | 18 US-10-717-282-7 | Sequence 7, Appli |
| 7 | 2282.6 | 95.8 | 4477 | 20 US-10-842-006-1 | Sequence 1, Appli |

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|----|--------|------|------|----|---------------------|--------------------|
| 8 | 2282.6 | 95.8 | 4477 | 20 | US-10-608-449-1 | Sequence 1, Appli |
| 9 | 2218.6 | 93.1 | 2786 | 10 | US-09-863-818A-9 | Sequence 9, Appli |
| 10 | 2218.6 | 93.1 | 2786 | 19 | US-10-749-144-9 | Sequence 9, Appli |
| 11 | 2218.6 | 93.1 | 2786 | 21 | US-10-924-667-9 | Sequence 9, Appli |
| 12 | 2215.4 | 93.0 | 3083 | 9 | US-09-809-567-1 | Sequence 1, Appli |
| 13 | 2215.4 | 93.0 | 3083 | 14 | US-10-216-156-1 | Sequence 1, Appli |
| 14 | 2215.4 | 93.0 | 3083 | 18 | US-10-616-788-1 | Sequence 3, Appli |
| 15 | 2215.4 | 93.0 | 3083 | 20 | US-10-842-006-3 | Sequence 3, Appli |
| 16 | 2158.4 | 90.6 | 4392 | 14 | US-10-343-348-15 | Sequence 15, Appli |
| 17 | 2128 | 89.3 | 2894 | 17 | US-10-104-047-1429 | Sequence 1429, Ap |
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| 22 | 2074.2 | 87.0 | 2319 | 13 | US-10-000-157-17 | Sequence 17, Appli |
| 23 | 2074.2 | 87.0 | 2319 | 16 | US-10-410-927-17 | Sequence 17, Appli |
| 24 | 2074.2 | 87.0 | 2319 | 16 | US-10-410-374-17 | Sequence 17, Appli |
| 25 | 2074.2 | 87.0 | 2319 | 16 | US-10-410-552-17 | Sequence 17, Appli |
| 26 | 2074.2 | 87.0 | 2319 | 17 | US-10-458-442-17 | Sequence 17, Appli |
| 27 | 2074.2 | 87.0 | 2319 | 18 | US-10-408-385-17 | Sequence 17, Appli |
| 28 | 2070.4 | 86.9 | 4450 | 21 | US-10-477-714-42 | Sequence 42, Appli |
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| 30 | 1638.4 | 68.8 | 2443 | 9 | US-09-912-157-11 | Sequence 11, Appli |
| 31 | 1638.4 | 68.8 | 2443 | 18 | US-10-717-282-11 | Sequence 11, Appli |
| 32 | 1614.2 | 67.7 | 2259 | 9 | US-09-912-157-3 | Sequence 3, Appli |
| 33 | 1614.2 | 67.7 | 2259 | 18 | US-10-717-282-3 | Sequence 3, Appli |
| 34 | 1612 | 67.6 | 2259 | 9 | US-09-912-157-6 | Sequence 6, Appli |
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| 36 | 1532 | 64.3 | 2217 | 9 | US-09-912-157-9 | Sequence 9, Appli |
| 37 | 1532 | 64.3 | 2217 | 18 | US-10-717-282-9 | Sequence 9, Appli |
| 38 | 1322.4 | 55.5 | 2217 | 18 | US-09-912-157-13 | Sequence 13, Appli |
| 39 | 1322.4 | 55.5 | 2217 | 18 | US-10-717-282-13 | Sequence 13, Appli |
| 40 | 743 | 31.2 | 1723 | 18 | US-10-616-788-18 | Sequence 18, Appli |
| 41 | 393.2 | 16.5 | 453 | 10 | US-09-918-995-26425 | Sequence 26425, A |
| 42 | 71.4 | 3.0 | 3120 | 15 | US-10-207-555-106 | Sequence 106, App |
| 43 | 71.4 | 3.0 | 3120 | 19 | US-10-717-597-84 | Sequence 84, Appli |
| 44 | 71.4 | 3.0 | 3120 | 21 | US-10-505-680-584 | Sequence 584, App |
| 45 | 71.4 | 3.0 | 3223 | 19 | US-10-742-161-9 | Sequence 9, Appli |

ALIGNMENTS

RESULT 1
US-09-912-157-1
; Sequence 1, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
US-09-912-157-1

Query Match 100.0%; Score 2383; DB 9; Length 2383;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CGCGCGCGCCACCGCCCACTCGGGGCTGGCCAGCGGGCGGGCGCGAGAAC 60


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RESULT 4

US-10-717-282-4

; Sequence 4, Application US/10717282

; Publication No. US20040077052A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10/717,282

; CURRENT FILING DATE: 2003-11-19

; PRIOR APPLICATION NUMBER: US/09/912,157

; PRIOR FILING DATE: 2001-07-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 2383

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (86)...(2344)

US-10-717-282-4

Query Match 99.7%; Score 2376.6; DB 18; Length 2383;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 CCGCGCGGCGCACCGCCCACTCGGGGTGGCCAGCGGCGGCGCGCGGCGGCGAGAGAAC 60
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Db 61 GGCCTGGTGGCGGAGCGCACGGCCATGCCCCCGTGGCTGAGCTCTGCTCGCTTCTT 120
Oy 121 TACGCTCAACCCCTGCTCAACGGCTCGAGCTGCTGCGCTGCGCGGTCCGGCGG 180
Db 121 TACGCTCAACCCCTGCTCAACGGCTCGAGCTCGAGCTCGAGCTGCGCGGTCCGGCGG 180
Oy 181 CCGCGGCGGCGCGACACCTGTGGCTGAGGATGAAAGCGGCTGCCGAGCCCGGCTTTG 240
Db 181 CCGCGGCGGCGCGACACCTGTGGCTGAGGATGAAAGCGGCTGCCGAGCCCGGCTTTG 240
Oy 241 TGTTCCTAATGAGGAGTGGGCGCAGCCAGAGAAAGAGTGGGCTGTACACATCACCTT 300
Db 241 TGTTCCTAATGAGGAGTGGGCGCAGCCAGAGAAAGAGTGGGCTGTACACATCACCTT 300
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QY 301 CAAATATGACAAATTGTTACCACTACTTGAATCCAGTGGGAAGCATGTGATTGCTGAGCG 360
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QY 361 CCAGAAATATCAACCATCAGCCAGTAGTGTGTCATGACCAAGTGGCAGTCAACATTTCTTTG 420
DB 361 CCAGAAATATCAACCATCAGCCAGTAGTGTGTCATGACCAAGTGGCAGTCAACATTTCTTTG 420
QY 421 GTCCCGAGGGCCCTCGGCATCGAATTTCTGAAAGGATTTCCGGTAAATACATGGAAGGACT 480
DB 421 GTCCCGAGGGCCCTCGGCATCGAATTTCTGAAAGGATTTCCGGTAAATACATGGAAGGACT 480
QY 481 GAAGTCGAGGGAAGACAGTGCACACACTGATTTCTTAAAGGATCCGAAGCAGCTCAACAG 540
DB 481 GAAGTCGAGGGAAGACAGTGCACACACTGATTTCTTAAAGGATCCGAAGCAGCTCAACAG 540
QY 541 TAGCTTCAAAAGAACTGGAATCGAATCTCAACCTTTCTGTAATATGAAATTTGAAACGGA 600
DB 541 TAGCTTCAAAAGAACTGGAATCGAATCTCAACCTTTCTGTAATATGAAATTTGAAACGGA 600
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DB 661 CTCTCTTAGAACCGAGCTGTGACCTGTTGTACAGCCGACAACTTAGCTTGTAAACC 720
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DB 721 CTCTCGGAAGCTCGGAACCTGAACTCAGCCAGCATGGCTCGGACATGCAAGTGTCTTT 780
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DB 781 CGACATGCAACGCAAACTTCGGCTTCGGTTCCTTCTTATTTCACTAAGCTCAAGCA 840
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DB 841 CGAGGACCTTTCAGCGAAGACTGTGACGAGGCAAACTACAGAGCAGCACGCTG 900
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DB 1261 CTACTTCTCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAG 1320
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DB 1321 CCTCTGTAGAGAGGCGCAGAGAGATGGGTCAATCCAGAAAGATCCACGAGTCCCAAGTTCA 1380

QY 1381 CATTTGTTGTTGTTTCCAAAGGTATGAAGTACTTTGTGGAACAAGAACTTACAAACAA 1440
DB 1381 CATTTGTTGTTGTTTCCAAAGGTATGAAGTACTTTGTGGAACAAGAACTTACAAACAA 1440
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DB 1441 AGGAGTGGCGAGGCTCGGGGAAAAGGAGAGCTCTTCTGTTGGCGGTGTGAGGCATTCG 1500
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DB 1501 CGAAAGCTCGCCAGGCCAAGCAGAGTTCGTCCGCGCGCTCAGCAAGTTTATTCGCCGT 1560
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QY 1741 AGGCCGCTCCCTATACGTGCGCAATTTGCAACATGCAACAGTTTATTTGACAGGAGCCCGA 1800
DB 1741 AGGCCGCTCCCTATACGTGCGCAATTTGCAACATGCAACAGTTTATTTGACAGGAGCCCGA 1800
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DB 1801 CTGTTTCCAAAGCAGTTGTTTCCCTTCCATCTTCCACTGCGCTACCCGGAGCCAGT 1860
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DB 1861 CTTGAGAAATTTGATTTGGGCTTGGTTTAAATGATGTCAATGTGCAAAACAGAGCCCTGA 1920
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DB 1921 GAGTGACTTTCGCTTAAAGGTAGAGGGGCTGTTTCTTTGGGGCAACCGGACAGCCGACTC 1980
QY 1981 CCAGCACAGAGTCAAGTGGGGCTGGACCAAGACGGGAGGCGCGGCTGCGCTTTGA 2040
DB 1981 CCAGCACAGAGTCAAGTGGGGCTGGACCAAGACGGGAGGCGCGGCTGCGCTTTGA 2040
QY 2041 CGGTAGCGCCGCTGCAACCCCTGCTGCAACCGTGAAGCGCGAGCCCTCGGACAT 2100
DB 2041 CGGTAGCGCCGCTGCAACCCCTGCTGCAACCGTGAAGCGCGAGCCCTCGGACAT 2100
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DB 2101 GCCCGGGAATTCAGGCATCTATGACTGCTGTGCTGCTCATTCGAGCTGTCTCTGCCACT 2160
QY 2161 GATGGAAGGACTCTCGACGGAACAGAGAAACGTTCTTCTCTGACGGAGAGGCTGTCTC 2220
DB 2161 GATGGAAGGACTCTCTCGACGGAACAGAGAAACGTTCTTCTCTGACGGAGAGGCTGTCTC 2220
QY 2221 CTCTTTCAGGCTGGGTGAGGAGAACTTCTGCGCTTCTTCCAGCTCTCTCTCTG 2280
DB 2221 CTCTTTCAGGCTGGGTGAGGAGAACTTCTGCGCTTCTTCCAGCTCTCTCTCTG 2280
QY 2281 GTCATGCAAAAGCAGATCTTGGTTCGCGAGCTACATGATGAACCTCAACGCGGTCGCCCC 2340
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QY 2341 TTTGTAAACAAACGAAAGAGTCTAAGCAATTGCCACTTTTAGCTG 2383
DB 2341 TTTGTAAACAAACGAAAGAGTCTAAGCAATTGCCACTTTTAGCTG 2383

RESULT 5

US-09-912-157-7

; Sequence 7, Application US/09912157

; Patent No. US20020165348A1


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Db 1879 GAGTGACTTTCCTTAAAGGTAGAGGCGGTGTTCTTGGGGCAACCGGACAGCGGACTC 1938
QY 1981 CCAGCACGAGAGTCAGCATGCGGGCTTGGAACAAAGAGGGGAGGCCCGGCTCGGACAT 2040
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QY 2041 CGGTAGCGCCCTCTGCAACCCCTGCTGCAACCGGTGAAAGCGGCGCCCTCGGACAT 2100
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QY 2341 TTTGTAAACAAACGAAAGAGTCTAAGCATTCGCCACTTTAGCTG 2383
Db 2299 TTTGTAAACAAACGAAAGAGTCTAAGCATTCGCCACTTTAGCTG 2341
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US-10-717-282-7
; Sequence 7, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Fresnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2302)
US-10-717-282-7
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Query Match 96.1%; Score 2289; DB 18; Length 2341;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2341; Conservative 0; Mismatches 0; Indels 42; Gaps 1;
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QY 61 GGCCTGGCTGGCGGAGCGCAGCGGCATGGCCCGTGGCTGGAGCTCTGCTCCGCTCTTCTT 120
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QY 481 GAAGTCGGAGGGAAGACAGTGCACAACTGATTTCTAAAGATCCGAGCAGCTCAACAG 540
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QY 1021 CAGAGCGGTGGCCATCAGGTGCCACTGATGTCATATCGGCATTTCCGACGCTCTTCCAC 1080
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QY 1141 TGAGTCTTCCACATACATGTCAGCACTCCCAAGAGAGAGGCTCCGGCGCGCGCGCAAGGT 1200
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Qy 1681 CCAGAGCCGGGCGAGCACGCGAGAGGCGAGAGAACTACTTCCGAGCAAGTC 1740
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Db 1699 AGGCGGTCCCTATACGTGCGCATTTGCAACATGCAACAGTTTATGACAGGAGCCCGA 1758
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Db 1819 CTTGAGAGAAATTTGATTCGGGCTTGCTTTTAAATGATGTCATGTCGCAACAGGCGCTGA 1878
Qy 1921 GAGTGACTTCTGCTTAAAGGTAGAGCGGCTGTTCTTGGGGCAACCGGACAGCGGACTC 1980
Db 1879 GAGTGACTTCTGCTTAAAGGTAGAGCGGCTGTTCTTGGGGCAACCGGACAGCGGACTC 1938
Qy 1981 CCAGACGAGAGTCAAGCATGGGGGCTTGACCAAGACGCGGAGGCGCCGCTGCTCCTTGA 2040
Db 1939 CCAGACGAGAGTCAAGCATGGGGGCTTGACCAAGACGCGGAGGCGCCGCTGCTCCTTGA 1998
Qy 2041 CGGTAGCGCGGCTTGCAACCTCTGTCGACACGCGTGAAGCCGCGAGCCCTCGGACAT 2100
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Db 2119 GATGAAGGACTCTCGAGGACGACAGAGAACTCTTCCCTGACGAGAGCGTGTCTCTC 2178
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Db 2299 TTTCTAACAACCAAGAGTCTAAGCATTCGCCACTTTAGCTG 2341

RESULT 7
US-10-842-006-1
; Sequence 1, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruyi-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; FILE REFERENCE: MPI03-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(2309)
US-10-842-006-1

Query Match 95.8%; Score 2282.6; DB 20; Length 4477;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2337; Conservative 0; Mismatches 4; Indels 42; Gaps 1;

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Qy 361 CCAGAAATACCAATACAGCCAGTATGCTTGCCATGACCAAGTGGGAGTCACCAATCTTTG 420
Db 323 CCAGAAATACCAATACAGCCAGTATGCTTGCCATGACCAAGTGGGAGTCACCAATCTTTG 382
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Db 383 GTCCCCAGGGGCGCTCGGCATCGCAATTCCTGAAGGATTTCCGGTAAATCTGGAGAGCT 442
Qy 481 GAAGTCGAGGAGAGACAGTCCCAACTGATTTCTAAGGATCCGAGAGCTCAACAG 540
Db 443 GAAGTCGAGGAGAGACAGTCCCAACTGATTTCTAAGGATCCGAGAGCTCAACAG 502
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Qy 721 CTCTGGAAGCCTCGAAGCCTGAACATCAGCCAGCATGCTCGACATGCAAGTGTCTTT 780
Db 683 CTCTGGAAGCCTCGAAGCCTGAACATCAGCCAGCATGCTCGAATGCAAGTGTCTTT 742
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Qy 1141 TGAGTCTTCCACATACATCGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGGCCGGAAGGT 1200
Db 1103 TGAGTCTTCCACATACATCGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGGCCGGAAGGT 1162
Qy 1201 CTCTTCTCTGCTATTTCAGTAAAGATGCGCCAGAAATCAGATGAATGCTGTCAGTGTTCGC 1260
Db 1163 CTCTTCTCTGCTATTTCAGTAAAGATGCGCCAGAAATCAGATGAATGCTGTCAGTGTTCGC 1222
Qy 1261 CTACTTCTCCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAG 1320
Db 1223 CTACTTCTCCAGGACTTCTGTGGCTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAG 1282
Qy 1321 CCTCTGTAGAGAAGGCGCAGAGAAATGGTTCATCCAGAAGATCCACGAGTCCCAGTTTCAT 1380
Db 1283 CCTCTGTAGAGAAGGCGCAGAGAAATGGTTCATCCAGAAGATCCACGAGTCCCAGTTTCAT 1342
Qy 1381 CATTTGTGTTTGTTCGAAAGGTATGAAGTACTTTGTGACAGAAAGAACTACAAACACAA 1440
Db 1343 CATTTGTGTTTGTTCGAAAGGTATGAAGTACTTTGTGACAGAAAGAACTACAAACACAA 1402
Qy 1441 AGGAGGTGGCGAGGCTCGGGGAAAGGAGAGCTCTTCTGTTGGCGGTGTGAGCCATTGC 1500
Db 1403 AGGAGGTGGCGAGGCTCGGGGAAAGGAGAGCTCTTCTGTTGGCGGTGTGAGCCATTGC 1462
Qy 1501 CGAAAAGTCTCCGCCAGGCGCAAGCAGAGTTCGTTCGCGCGGCTCGACCAAGTTTATCGCCGT 1560
Db 1463 CGAAAAGTCTCCGCCAGGCGCAAGCAGAGTTCGTTCGCGCGGCTCGACCAAGTTTATCGCCGT 1522
Qy 1561 CTACTTTGATTTATTCCTCGAGGGGAGAGCTCCCGGGTATCTAGACCTGAGTACCAAGTA 1620
Db 1523 CTACTTTGATTTATTCCTCGAGGGGAGAGCTCCCGGGTATCTAGACCTGAGTACCAAGTA 1582
Qy 1621 CAGACTCATGGACAATCTTCTCAGCTCTGTTCCTCCACTTGCACCTCCCGAGACCAGGCGCT 1680
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Db 1583 CAGACTCATGGACAATCTTCTCAGCTCTGTTCCCACTCTGCACCTCCGAGACCAGGCGCT 1642
Qy 1681 CCAGGAGCCGGGAGCAGACACGCGACAGGGCAGAGAGAACTACTTCCGGAGCAAGTC 1740
Db 1643 CCAGGAGCCGGGAGCAGACACGCGACAGGGCAGAGAGAACTACTTCCGGAGCAAGTC 1702
Qy 1741 AGGCGGTCCCTATACGTCGCTCCATTTGCAACATGCACAGTTTATTGACAGAGAGCCGGA 1800
Db 1703 AGGCGGTCCCTATACGTCGCTCCATTTGCAACATGCACAGTTTATTGACAGAGAGCCGGA 1762
Qy 1801 CTGTTTCCGAAAAGCAGTTCGTTCCCTTCCATTCCTCCTCCACTGCGCTACCGGAGCCAGT 1860
Db 1763 CTGTTTCCGAAAAGCAGTTCGTTCCCTTCCATTCCTCCTCCACTGCGCTACCGGAGCCAGT 1822
Qy 1861 CTTGAGAAATTTGATTTGGGCTTGGTTTAAATGATGTCATGTGCAAAACGAGGCGCTGA 1920
Db 1823 CTTGAGAAATTTGATTTGGGCTTGGTTTAAATGATGTCATGTGCAAAACGAGGCGCTGA 1882
Qy 1921 GAGTGACTTCTGCTTAAAGGTAGAGGCGGTGTTCTTTGGGGCAACCGGACCCAGCGACTC 1980
Db 1883 GAGTGACTTCTGCTTAAAGGTAGAGGCGGTGTTCTTTGGGGCAACCGGACCCAGCGACTC 1942
Qy 1981 CCAGCACGAGAGTCAGCATGCGGCGCTTGGACCAAGACGCGGAGGCCCGGCTGCTTGA 2040
Db 1943 CCAGCACGAGAGTCAGCATGCGGCGCTTGGACCAAGACGCGGAGGCCCGGCTGCTTGA 2002
Qy 2041 CGGTAGCGCGCCTCGCAACCCCTGTGTCACACCGGTGAAGCCGGACGCCCTCGACAT 2100
Db 2003 CGGTAGCGCGCCTCGCAACCCCTGTGTCACACCGGTGAAGCCGGACGCCCTCGACAT 2062
Qy 2101 GCCGCGGACTCAGGCATCTATGACTGTCTGTGCCCTCATCCGAGCTGTCTTGCCTACT 2160
Db 2063 GCCGCGGACTCAGGCATCTATGACTGTCTGTGCCCTCATCCGAGCTGTCTTGCCTACT 2122
Qy 2161 GATGGAAGGACTCTCGACGGAACCAAGACAGAAACGCTTTCCTGACGAGAGCGTGTCTC 2220
Db 2123 GATGGAAGGACTCTCGACGGAACCAAGACAGAAACGCTTTCCTGACGAGAGCGTGTCTC 2182
Qy 2221 CTCTTAGGCGCTGGGTAGAGGAACTCTGCGCCCTTCTTCCAGCTCTCTTCTTGG 2280
Db 2183 CTCTTAGGCGCTGGGTAGAGGAACTCTGCGCCCTTCTTCCAGCTCTCTTCTTGG 2242
Qy 2281 GTCATGCAAAAGCAGATCTTGGTTCCCGCAGCTACACTGATGAACTCCACGCGGTGCGCCC 2340
Db 2243 GTCATGCAAAAGCAGATCTTGGTTCCCGCAGCTACACTGATGAACTCCACGCGGTGCGCCC 2302
Qy 2341 TTTGTAAACAAACGAAAGAGTCTAAGCATTCGCCACTTTAGCTG 2383
Db 2303 TTTGTAAACAAACGAAAGAGTCTAAGCATTCGCCACTTTAGCTG 2345
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RESULT 8
US-10-608-449-1
; Sequence 1, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: I2003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-449-1

Query Match 95.8%; Score 2282.6; DB 20; Length 4477;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 2337; Conservative 0; Mismatches 4; Indels 42; Gaps 1;

QY 1 CGCGCGCGCCACCGCCCACTCGGGCTGGCCAGCGCGGGCGGCGCGGGCGCGAGAGAAC 60
DB |||||
5 CGCGCGCGCGCCACCGCCCACTCGGGCTGGCCAGCGCGGCGGGCGCGGGCGCGAGAGAAC 64
QY 61 GGCCTGGCTGGCGAGCGGCAAGCGCATCGGCCCGGTGGCTGCAAGCTCTGCTCGCTTCTT 120
DB |||||
65 GGCCTGGCTGGCGAGCGGCAAGCGCATCGGCCCGGTGGCTGCAAGCTCTGCTCGCTTCTT 124
QY 121 TACGGTCAACGCTGCTCAACGGCTCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 180
DB |||||
125 TACGGTCAACGCTGCTCAACGGCTCGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 184
QY 181 CGCGCGCGCGCGGACACCTGCTGGCTGGAGGATGAAGCGGCTGCCCGACCGCGCTTTG 240
DB |||||
185 CGCGCGCGCGCGGACACCTGCTGGCTGGAG----- 214
QY 241 TGTGCTTAATGAGGAGTGGGCGCAGCGAGCAAGAAACAGTGGCTGTGAACATCACCTT 300
DB |||||
215 -----GGAGTGGGCGCAGCGCAGCAAGAAACAGTGGCTGTGAACATCACCTT 262
QY 301 CAATATGCAATTTGACCACTACTGTAATCCAGTGGGAGCATGTGATTGCTGACGC 360
DB |||||
263 CAATATGCAATTTGACCACTACTGTAATCCAGTGGGAGCATGTGATTGCTGACGC 322
QY 361 CCAGAAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTTCTTTG 420
DB |||||
323 CCAGAAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCATTTCTTTG 382
QY 421 GTCCCCAGGGGCTCGGCATCGAATCTCTGAAGGATTTGGGTAAATCTGGAGAGCT 480
DB |||||
383 GTCCCCAGGGGCTCGGCATCGAATCTCTGAAGGATTTGGGTAAATCTGGAGAGCT 442
QY 481 GAACTCGAGGGAAGACAGTGGCAACACTGATTTCTAAAGNATCGAAGCAGCTCAACAG 540
DB |||||
443 GAACTCGAGGGAAGACAGTGGCAACACTGATTTCTAAAGNATCGAAGCAGCTCAACAG 502
QY 541 TAGCTTCAAAAGAACTGGAAATGGAATCTCAACCTTTCTGAAATGAAATTTGAAACGGA 600
DB |||||
503 TAGCTTCAAAAGAACTGGAAATGGAATCTCAACCTTTCTGAAATGAAATTTGAAACGGA 562
QY 601 TTATTTGTAAGGTTGTCCCTTTTCTTCCATTAATAAAGCAATTAACACCTTT 660
DB |||||
563 TTATTTGTAAGGTTGTCCCTTTTCTTCCATTAATAAAGCAATTAACACCTTT 622
QY 661 CTTCTTTAGAACCGAGCTGTGACTGTGTTGTTACAGCGGACATCTAGCTTTGTAACC 720
DB |||||
623 CTTCTTTAGAACCGAGCTGTGACTGTGTTGTTACAGCGGACATCTAGCTTTGTAACC 682
QY 721 CTTCTGGAAGCTCGGAACCTGAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTT 780
DB |||||
683 CTTCTGGAAGCTCGGAACCTGAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTT 742
QY 781 CGACCATGCAACCGCAACTTCGGCTTCGGTTTCTTCTATCTTCACTCAAGCTCAAGCA 840
DB |||||
743 CGACCAACCGCAACCTTCGGCTTCGGTTTCTTCTATCTTCACTCAAGCTCAAGCA 802
QY 841 CGAAGCACTTTCAAGCGAAGACCTGTAAAGCAGGAGCAAACTACAGAGACGACAGCTG 900
DB |||||
803 CGAAGCACTTTCAAGCGAAGACCTGTGAGCAGGAGCAAACTACAGAGATGACCAAGCTG 862
QY 901 CTTCTTCAAAATGTTTCTCAGGGGATTTATATATGAGCTGTGGATGACACTTAACAC 960
DB |||||
863 CTTCTTCAAAATGTTTCTCAGGGGATTTATATATGAGCTGTGGATGACACTTAACAC 922
QY 961 AACAGAAAAGTGATGCTATTATGCTTAAAGCAGTGCACTCCCGTGGCGCGGCCCAT 1020
DB |||||
923 AACAGAAAAGTGATGCTATTATGCTTAAAGCAGTGCACTCCCGTGGCGCGGCCCAT 982
QY 1021 CAGACCGGTGGCCATCACAAGTGGCACTGGTAGTGCATATCGGCATTTCCGAGCGCTTTCAC 1080
DB |||||
983 CAGACCGGTGGCCATCACAAGTGGCCATGCTAGTAGTGCATATCGGCATTTCCGAGCGCTTTCAC 1042

QY 1081 TGTGATGTGCGCGCAAGAGCAACAAAGAAATATATATTTCACTTTAGATGAAGAGAGCTC 1140
DB |||||
1043 TGTGATGTGCGCGCAAGAGCAACAAAGAAATATATATTTCACTTTAGATGAAGAGAGCTC 1102
QY 1141 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGCGCGCAAGGT 1200
DB |||||
1103 TGAGTCTTCCACATACACTGCAGCACTCCCAAGAGAGAGGCTCCGGCGCGCGCGCAAGGT 1162
QY 1201 CTTTCTCTGCTATTTCCAGTAAAGATGGCCAGAATCACAATGATGTGCTCCAGTGTTCGC 1260
DB |||||
1163 CTTTCTCTGCTATTTCCAGTAAAGATGGCCAGAATCACAATGATGTGCTCCAGTGTTCGC 1222
QY 1261 CTACTTCTCAGGACTTCTGTGGCTGTGAGGTGGCTCTGGAACCTGTGCGGAAGACTTCAG 1320
DB |||||
1223 CTACTTCTCAGGACTTCTGTGGCTGTGAGGTGGCTCTGGAACCTGTGCGGAAGACTTCAG 1282
QY 1321 CCTGTGTAAGAGGCGCAGAGAGATGGGTCAATCCAGAAGATCCACAGTCCCAGTTCAT 1380
DB |||||
1283 CCTGTGTAAGAGGCGCAGAGAGATGGGTCAATCCAGAAGATCCACAGTCCCAGTTCAT 1342
QY 1381 CATTTGTGTTTGTTCAAAAGGTATGAAGTACTTTGTGCAAGAGAACTTACAAACACAA 1440
DB |||||
1343 CATTTGTGTTTGTTCAAAAGGTATGAAGTACTTTGTGCAAGAGAACTTACAAACACAA 1402
QY 1441 AGGAGGTGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGTGGCGGTGTGAGCCATTGC 1500
DB |||||
1403 AGGAGGTGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGTGGCGGTGTGAGCCATTGC 1462
QY 1501 CGAAAAGCTCCGCGCAGGCAAGCAGAGTTCTGTCGCGCGCTCAGCAAGTTTATCGCGT 1560
DB |||||
1463 CGAAAAGCTCCGCGCAGGCAAGCAGAGTTCTGTCGCGCGCTCAGCAAGTTTATCGCGT 1522
QY 1561 CTACTTTGATTATTTCTGCGAGGAGAGCTCCCGGTATCTTAGACTGTAGTACCAAGTA 1620
DB |||||
1523 CTACTTTGATTATTTCTGCGAGGAGAGCTCCCGGTATCTTAGACTGTAGTACCAAGTA 1582
QY 1621 CAGACTCATGACAAATCTTCTCAGCTCTGTTCCACTTGTGCACTCCCGAGACCAAGCT 1680
DB |||||
1583 CAGACTCATGACAAATCTTCTCAGCTCTGTTCCACTGCTCCAGACCAAGCT 1642
QY 1681 CGAGAGCGGGGCGAGCACACCGCAGGCGAGGAGGAGAACTACTTCCGAGGAGCTC 1740
DB |||||
1643 CGAGAGCGGGGCGAGCACACCGCAGGCGAGGAGGAGAACTACTTCCGAGGAGCTC 1702
QY 1741 AGGCGGTCTCTATACGTGCGCATTTGCAACATGCAACAGTTTATGACAGGAGCGCA 1800
DB |||||
1703 AGGCGGTCTCTATACGTGCGCATTTGCAACATGCAACAGTTTATGACAGGAGCGCA 1762
QY 1801 CTGTTTGAAGAGCAGTTCTGTTCCCTCTCTCTCCACTGCTACCGGAGCGAGT 1860
DB |||||
1763 CTGTTTGAAGAGCAGTTCTGTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1822
QY 1861 CTGAGGAAATTTGATTCGGGCTTGGTTTAAATGATGTCTGTCGAACCGAGGCGCTGA 1920
DB |||||
1823 CTGAGGAAATTTGATTCGGGCTTGGTTTAAATGATGTCTGTCGAACCGAGGCGCTGA 1882
QY 1921 GAGTGACTTCTGCTTAAAGGTAGAGCGGCTGTTCTTGGGGCAACCGGACCGAGCTC 1980
DB |||||
1883 GAGTGACTTCTGCTTAAAGGTAGAGCGGCTGTTCTTGGGGCAACCGGACCGAGCTC 1942
QY 1981 CCAGCAAGAGTCAAGTGGGGGCTTGGAACAGACCGGGAGGCGCGGCTGCTTGA 2040
DB |||||
1943 CCAGCAAGAGTCAAGTGGGGGCTTGGAACAGACCGGGAGGCGCGGCTGCTTGA 2002
QY 2041 CGGTAGCGCGCTTGGAACCGCTCTGTCACACGCTGAAGCGCGGAGCCCTCCGACAT 2100
DB |||||
2003 CGGTAGCGCGCTTGGAACCGCTCTGTCACACGCTGAAGCGCGGAGCCCTCCGACAT 2062
QY 2101 GCCGCGGACTCAGGCACTTATGACTGTGTGCGCTCATCCGAGCTGTCTCTGCACT 2160
DB |||||
2063 GCCGCGGACTCAGGCACTTATGACTGTGTGCGCTCATCCGAGCTGTCTCTGCACT 2122
QY 2161 GATGGAAGACTCTCGACGGAACAGACAGAAACGCTCTTCTCTGACGAGAGCGTGTCTC 2220

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Db 2123 GATGGAAGACTCTCGACGGACACAGAGAAAGCTTCCCTGACGGAGAGCGGTGCTCTC 2182
Qy 2221 CTCTTCAGCCCTGGGTGAGAGAGAACCTCCCTGCGCCCTCTTCCAAAGCTCCTCTCTTGG 2280
Db 2183 CTCTTCAGCCCTGGGTGAGAGAGAACCTCCCTGCGCCCTCTTCCAAAGCTCCTCTCTTGG 2242
Qy 2281 GTCAATGCAACAGATCTTGGTGTGCGCAGCTACACTGATGAATCCACGCGGTGCGCCC 2340
Db 2243 GTCAATGCAACAGATCTTGGTGTGCGCAGCTACACTGATGAATCCACGCGGTGCGCCC 2302
Qy 2341 TTGTGTAAACAAACGAAAGAGTCTAAGCATTTGCCACTTTAGCTG 2383
Db 2303 TTGTGTAAACAAACGAAAGAGTCTAAGCATTTGCCACTTTAGCTG 2345

RESULT 9
US-09-863-818A-9
; Sequence 9, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(2283)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (118)..( )
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (194)..(194)
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; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-09-863-818A-9
Query Match 93.1%; Score 2218.6; DB 10; Length 2786;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 20; Indels 45; Gaps 2;
Qy 27 CTGGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 86
Db 11 CGGGCCAGCAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 70
Qy 87 TGGCCCCGTGGTGCAGCTCTGCTCCGTCCTTTTACGGTCAACGCTGCTCAACGCTGCTCAACGCGCT 146
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Db 71 TGGCCCCGTGGTGCAGCTCTGCTCCGTCCTTTTACGGTCAACGCTGCTGCTCAACGCGCT 130
Qy 147 CGCAGCTGGCTGTGGCGCGCTGGCGGGTCCGGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 206
Db 131 CGCAGCTGGCTGTGGCGGGTCCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 190
Qy 207 GGAGGATGAAAGCGGCTGCCGACCCCGGCTTTGTGTCTTAATGAGGAGTGGGGCCAG 266
Db 191 GGA-----NGGGAGTGGGGCCAG 208
Qy 267 CCAGCAGAAACAGTGGGCTGTGTAACAATCACTTTCAAATATGACAAATGTGTACCACTACT 326
Db 209 CCAGCAGAAACAGTGGGCTGTGTAACAATCACTTTCAAATATGACAAATGTGTACCACTACT 268
Qy 327 TGAATCCAGTGGGGAACATGTGTTGCTGAGCCCGAGAAATATCACCATCAGCCAGTATG 386
Db 269 TGAATCCAGTGGGGAACATGTGTTGCTGAGCCCGAGAAATATCACCATCAGCCAGTATG 328
Qy 387 CTTGCCATGACCAAGTGCAGTCAACCATTTCTTGTCCCGAGGGGCCCTCGGCATCGAAT 446
Db 329 CTTGCCATGACCAAGTGCAGTCAACCATTTCTTGTCCCGAGGGGCCCTCGGCATCGAAT 388
Qy 447 TCCTGAAAGGATTTCCGGGTAACTACTGGAGGAGCTGAAGTCCGAGGGAGAGCAGTGCACAAC 506
Db 389 TCCTGAAAGGATTTCCGGGTAACTACTGGAGGAGCTGAAGTCCGAGGGAGAGCAGNGCCAAAC 448
Qy 507 AACTGATTTAAAGGATCCGAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 566
Db 449 AACTGATTTAAAGGATCCGAGCAGNTCAACAGTAGCTTCAAAAGAACTGGAATGGAAT 508
Qy 567 CTCAACCTTTCTCGAATATGAAATTTGAAACGGAATTTTCGTAAGGTTCTCCCTTTTC 626
Db 509 CTCAACCTTTCTCGAATATGAAATTTGAAACGGAATTTTCGTAAGG---TTGTCTTTT 565
Qy 627 CTTCCATTTAAACGAAAGCAATTTACCACCTTTCTTTTGAAGCCCGAGCCCTGTGACC 686
Db 566 CTTTCATTTAAACGAAAGCAATTTACCACCTTTCTTTTGAAGCCCGAGCCCTGTGACC 625
Qy 687 TGTGTTACAGCCGGACAACTAGCTTTGTAACCTTTCTGGAAGCCTCGGAACCTGACACA 746
Db 626 TGTGTTACAGCCGGACAACTAGCTTTGTAACCTTTCTGGAAGCCTCGGAACCTGACACA 685
Qy 747 TCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGACACCGCACAACTTCGGCT 806
Db 686 TCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGACCATGACACCGCACAACTTCGGCT 745
Qy 807 TCCGTTTCTTCTATCTTCACTCAAGCTCAAGCAAGGAGCCTTTCAAGCGAAAGACCT 866
Db 746 TCCGTTTCTTCTATCTTCACTCAAGCTCAAGCAAGGAGCCTTTCAAGCGAAAGACCT 805
Qy 867 GTAAGCAGGAGCAAACTACAGAGACGACAGCTGCTCTTCAAAATGTTTCTCCAGGGG 926
Db 806 GTAAGCAGGAGCAAACTACAGAGATGACAGCTGCTCTTCAAAATGTTTCTCCAGGGG 865
Qy 927 ATTATATAATTGAGCTGTGATGACACTACAACAAGAAAGTGTGATGATGCT 986
Db 866 ATTATATAATTGAGCTGTGATGACACTACAACAAGAAAGTGTGATGATGCT 925
Qy 987 TAAAGCCAGTGCATCTCCCGTGGGCGCGGCCCATCAGAGCCGTGGCCATCAAGTGCAC 1046
Db 926 TAAAGCCAGTGCATCTCCCGTGGGCGCGGCCCATCAGAGCCGTGGCCATCAAGTGCAC 985
Qy 1047 TGGTAGTCATATCGGCATTCGGACGCTCTTCACTGTGATGTGCGGCAAGCAACAG 1106
Db 986 TGGTAGTCATATCGGCATTCGGACGCTCTTCACTGTGATGTGCGGCAAGCAACAG 1045
Qy 1107 AAAATATATATTCATTTAGATGAAGAGACTCTGAGTCTTCCACATACACTGCAGCAC 1166
Db 1046 AAAATATATATTCATTTAGATGAAGAGACTCTGAGTCTTCCACATACACTGCAGCAC 1105
Qy 1167 TCCCAAGAGAGAGGCTCCGGCCGCGCGCGAAAGGTTTCTCTGCTATTTCAGTAAAGATG 1226
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Db 1106 TCCCAAGAGAGAGGCTCCGGCCCGCGCGAAGGTCCTTCTCTGCTATTTCACGATAAAGATG 1165
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Db 1166 GCAGAAATCACATGAATGTCGTCCAGTGTTCGCCTACTTCTCCAGAGACTTCTGTGGCT 1225
QY 1287 GTGAGTGGCTCTCGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAAGGCGAGAGAAAT 1346
Db 1226 GTGAGTGGCTCTCGGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAAGGCGAGAGAAAT 1285
QY 1347 GGGTCATCCAGAAGATCCACGAGTCCAGTTCATCATTTGTGTGTTTGTTCCTCAAGGTATGA 1406
Db 1286 GGGTCATCCAGAAGATCCACGAGTCCAGTTCATCATTTGTGTGTTTGTTCCTCAAGGTATGA 1345
QY 1407 AGTACTTGTGACAAAGAAAGAACTACAAACACAAAGGAGGTGCGGAGGCTCGGGAAG 1466
Db 1346 AGTACTTGTGACAAAGAAAGAACTACAAACACAAAGGAGGTGCGGAGGCTCGGGAAG 1405
QY 1467 GAGAGCTCTTCTGTGTGGCGGTGTTCAGCCATTGCCGAAAGCTCCGCCAGGCCCAAGCAGA 1526
Db 1406 GAGAGCTCTTCTGTGTGGCGGTGTTCAGCCATTGCCGAAAGCTCCGCCAGGCCCAAGCAGA 1465
QY 1527 GTTCGTCCGGCGCTCAGCAAGTTTATCCGCTCTACTTTGATTATTCCTCGAGGGAG 1586
Db 1466 GTTCGTCCGGCGCTCAGCAAGTTTATCCGCTCTACTTTGATTATTCCTCGAGGGAG 1525
QY 1587 AGTCCCGGTATCCCTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTCAGC 1646
Db 1526 AGTCCCGGTATCCCTAGACCTGAGTACCAAGTACAGACTCATGACAAATCTTCTCAGC 1585
QY 1647 TCTGTTCCCACTTGCACCTCCGAGACACCGGCTCCAGGAGCGGGCGGAGCACAGCGAC 1706
Db 1586 TCTGTTCCCACTTGCACCTCCGAGACACCGGCTCCAGGAGCGGGCGGAGCACAGCGAC 1645
QY 1707 AGGGCAGCAGAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTATACGTCGCCATTT 1766
Db 1646 AGGGCAGCAGAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTATACGTCGCCATTT 1705
QY 1767 GCAACATGACCAAGTTTATGAGGAGCGGAGCCGACTGGTTCGAAAGCAGTTCGTTCCCT 1826
Db 1706 GCAACATGACCAAGTTTATGAGGAGCGGAGCCGACTGGTTCGAAAGCAGTTCGTTCCCT 1765
QY 1827 TCCATCCTCTCCTCCTACCGGAGCCAGTCTTGAGGAAATTTGATTCGGGCTTG 1886
Db 1766 TCCATCCTCTCCTCCTACCGGAGCCAGTCTTGAGGAAATTTGATTCGGGCTTG 1825
QY 1887 TTTTAAATGATGTCATGCAACACGAGGCTGAGAGTGACTTTCGCTTAAAGGTAGAG 1946
Db 1826 TTTTAAATGATGTCATGCAACACGAGGCTGAGAGTGACTTTCGCTTAAAGGTAGAG 1885
QY 1947 CGGCTGTTCTGGGGCAACCGGACGAGCCGACTCCCGACGACGAGTCAAGTGGGGCC 2006
Db 1886 CGGCTGTTCTGGGGCAACCGGACGAGCCGACTCCCGACGACGAGTCAAGTGGGGCC 1945
QY 2007 TGGACCAAGAGCGGAGGCGCGCTGCTTACGCTGAGCGCGCTGCAACCCCTGC 2066
Db 1946 TGGACCAAGAGCGGAGGCGCGCTGCTTACGCTGAGCGCGCTGCAACCCCTGC 2005
QY 2067 TGCACACGCTGAAAGCGGAGCGGCTCGGACATGCGCGGGACTCAGGCATCTATGAT 2126
Db 2006 TGCACACGCTGAAAGCGGAGCGGCTCGGACATGCGCGGGACTCAGGCATCTATGAT 2065
QY 2127 CGTCTGCTCCCTCATCCGAGCTGCTTCCGACATGAGGAGTCTGAGCGGACCA 2186
Db 2066 CGTCTGCTCCCTCATCCGAGCTGCTTCCGACATGAGGAGTCTGAGCGGACCA 2125
QY 2187 CAGAAAGCTTCTCCCTGACGAGAGGCTGCTCTTCCAGGCTGGGTGAGGAGAAC 2246
Db 2126 CAGAAAGCTTCTCCCTGACGAGAGGCTGCTCTTCCAGGCTGGGTGAGGAGAAC 2185
QY 2247 CTCTGCTCCCTTCTCCAAAGCTCCTCTCTTCTGGGTCAAGAGCAGATCTTGGTGGC 2306
Db 2186 CTCTGCTCCCTTCTCCAAAGCTCCTCTCTTCTGGGTCAAGAGCAGATCTTGGTGGC 2245

QY 2307 GCAGCTACACTGATGAATCCACGCGTCCGCCCTTTGTAAACAAACGAAAGAGTCTAAG 2366
Db 2246 GCAGCTACACTGATGAATCCACGCGTCCGCCCTTTGTAAACAAACGAAAGAGTCTAAG 2305
QY 2367 CATTCGCCACTTTAGCTG 2383
Db 2306 CATTCGCCACTTTAGCTG 2322

RESULT 10

US-10-749-144-9
; Sequence 9, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (70)..(2283)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (118)..()
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: unknown amino
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; LOCATION: (519)..(519)
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US-10-749-144-9

Query Match 93.1%; Score 2218.6; DB 19; Length 2786;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 2292; Conservative 0; Mismatches 20; Indels 45; Gaps 2;
QY 27 CTGGCCAGCGCGCGCGCGCGAGAACCGCCTGGCTGGCGGAGCGCACCGCCA 86
Db 11 CGGGCCAGCAGCGCGCGCGCGCGAGAACCGCCTGGCTGGCGGAGCGCACCGCCA 70
QY 87 TGGCCCGCGGTGCGAGCTCTGCTCGTCTCTTTACGGTCAACGCGCTCAACGGCT 146

[illegible]

| | | | |
|----|------|--|------|
| Db | 1106 | TCCCAAGAGAGAGGCTCCGGCCGGCGGAAGGTCTTTCTCTGTCTATTTCCAGCTAAAGATG | 1161 |
| Qy | 1227 | GCCAGAATCACATGAATGTGTCAGATGTTTTCCGCTACTTCTTCCAGGACTTCTGTGGCT | 1286 |
| Db | 1166 | GCCAGAATCACATGAATGTGTCAGATGTTTTCCGCTACTTCTTCCAGGACTTCTGTGGCT | 1225 |
| Qy | 1287 | GTGAGGTGGCTCTGGACCTGTGTGGGAAGACTTCAGCCTCTGTGTAGAAAGGGCAGAGAAAT | 1346 |
| Db | 1226 | GTGAGGTGGCTCTGGACCTGTGTGGGAAGACTTCAGCCTCTGTGTAGAAAGGGCAGAGAAAT | 1285 |
| Qy | 1347 | GGGTATCATCAGAAGATCCAGAGTCCAGTTCATCATTTGTTGTTTCCAAAGGTATCA | 1406 |
| Db | 1286 | GGGTATCATCAGAAGATCCAGAGTCCAGTTCATCATTTGTTGTTTCCAAAGGTATCA | 1345 |
| Qy | 1407 | AGTACTTTGTGGACAAGAACTACAAACAAAGGAGTGGCCGAGGCTCGGGGAAAG | 1466 |
| Db | 1346 | AGTACTTTGTGGACAAGAACTACAAACAAAGGAGTGGCCGAGGCTCGGGGAAAG | 1405 |
| Qy | 1467 | GAGAGCTCTTCTGTGTGGCGGTGTGACCCATTGCGAAAGGCTCCGCCAGGCCAAGCAGA | 1526 |
| Db | 1406 | GAGAGCTCTTCTGTGTGGCGGTGTGACCCATTGCGAAAGGCTCCGCCAGGCCAAGCAGA | 1465 |
| Qy | 1527 | GTTTCGTCCGGCGGCTCAGCAAGTTTATCGCGCTACTTTGATTTATTCCTCGAGGGAG | 1586 |
| Db | 1466 | GTTTCGTCCGGCGGCTCAGCAAGTTTATCGCGCTACTTTGATTTATTCCTCGAGGGAG | 1525 |
| Qy | 1587 | ACGTCCCGCGTATCTTAGACTCAGTACCAAGTACAGACTCATGGACAATCTTTCCTCAGC | 1646 |
| Db | 1526 | ACGTCCCGCGTATCTTAGACTCAGTACCAAGTACAGACTCATGGACAATCTTTCCTCAGC | 1585 |
| Qy | 1647 | TCTGTTCCCACTTGCACCTCCCGAGACACAGGCTCTCAGGAGCCGGGCGAGCACACGCGAC | 1706 |
| Db | 1586 | TCTGTTCCCACTTGCACCTCCCGAGACACAGGCTCTCAGGAGCCGGGCGAGCACACGCGAC | 1645 |
| Qy | 1707 | AGGCGACAGAGGAAGTACTTCCGAGCAGTACAGCCGGTCCCTATACGTGCGCATTT | 1766 |
| Db | 1646 | AGGCGACAGAGGAAGTACTTCCGAGCAGTACAGCCGGTCCCTATACGTGCGCATTT | 1705 |
| Qy | 1767 | GCAACATGCACAGTTTATTGACGAGGAGCCGACCTGGTTTCCGAAAGCAGTTTCGTTCCCT | 1826 |
| Db | 1706 | GCAACATGCACAGTTTATTGACGAGGAGCCGACCTGGTTTCCGAAAGCAGTTTCGTTCCCT | 1765 |
| Qy | 1827 | TCCATCTCTCTCCACTCGCGTACCCGGAGCCAGTCTTGAGAAATTTGATTCGGGCTTGG | 1886 |
| Db | 1766 | TCCATCTCTCTCCACTCGCGTACCCGGAGCCAGTCTTGAGAAATTTGATTCGGGCTTGG | 1825 |
| Qy | 1887 | TTTTAAATGATGTGTAATCCAGGCGCTGAGATGACTTCCTGCTTAAAGGTATAGG | 1946 |
| Db | 1826 | TTTTAAATGATGTGTAATCCAGGCGCTGAGATGACTTCCTGCTTAAAGGTATAGG | 1885 |
| Qy | 1947 | CGGCTGTTCTTTGGGGCAACCGGACCGGACTCCAGACACAGAGTTCAGCATTGGGGCC | 2006 |
| Db | 1886 | CGGCTGTTCTTTGGGGCAACCGGACCGGACTCCAGACACAGAGTTCAGCATTGGGGCC | 1945 |
| Qy | 2007 | TGGACCAAGACGGGAGGCCCGCTGCTGCTTGAACGGTACGCGCGCTTCGCAACCCCTGC | 2066 |
| Db | 1946 | TGGACCAAGACGGGAGGCCCGCTGCTGCTTGAACGGTACGCGCGCTTCGCAACCCCTGC | 2005 |
| Qy | 2067 | TGCACACGGTGAAGCGCGAGCCCTCGGACATGCGCGGGACTCAGGCATCTATGACT | 2126 |
| Db | 2006 | TGCACACGGTGAAGCGCGAGCCCTCGGACATGCGCGGGACTCAGGCATCTATGACT | 2065 |
| Qy | 2127 | CGTCTGTGCCCTCATCCGAGCTGTCTGTGCACTGATGGAAGGACTTCGACGCACAGA | 2186 |
| Db | 2066 | CGTCTGTGCCCTCATCCGAGCTGTCTGTGCACTGATGGAAGGACTTCGACGCACAGA | 2125 |
| Qy | 2187 | CAGAAAAGTCTTCCCTGACGGAGAGGTGCTCTCTTTAGGCGCTGGGTGAGGAGGAAC | 2246 |
| Db | 2126 | CAGAAAAGTCTTCCCTGACGGAGAGGTGCTCTCTTTAGGCGCTGGGTGAGGAGGAAC | 2185 |
| Qy | 2247 | CTCCTGCCCTTCTTCCAGTCTCTTCTTGGGTATGCAAGCAGATCTTGGTTGCC | 2306 |
| Db | 2186 | CTCCTGCCCTTCTTCCAGTCTCTTCTTGGGTATGCAAGCAGATCTTGGTTGCC | 2245 |

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| ; SEQ ID NO 1 | | | | | | | | | |
| ; LENGTH: 3083 | | | | | | | | | |
| ; TYPE: DNA | | | | | | | | | |
| ; ORGANISM: Homo sapiens | | | | | | | | | |
| ; FEATURE: | | | | | | | | | |
| ; NAME/KEY: CDS | | | | | | | | | |
| ; LOCATION: (22)..(2235) | | | | | | | | | |
| US-10-216-156-1 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 93.0%; Score 2215.4; DB 14; Length 3083; | | | | | | | | | |
| Matches 2271; Conservative 0; Mismatches 6; Indels 42; Gaps 1; | | | | | | | | | |
| Qy | 65 | TGGCTGGGCGAGCGCAGCGGCATGGCCCGGTGGCTGTGCGCTGTGCGCGGTGGCGCGCGG | 124 | | | | | | |
| Db | 1 | TGGCTGGGCGAGCGCAGCGGCATGGCCCGGTGGCTGTGCGCTGTGCGCGGTGGCGCGCGG | 60 | | | | | | |
| Qy | 125 | GTCAACGGCTGCTCAACGGCTGCGACGTGGCTGTGCGCGGTGGCGCGGTGGCGCGCGG | 184 | | | | | | |
| Db | 61 | GTCAACGGCTGCTCAACGGCTGCGACGTGGCTGTGCGCGGTGGCGCGGTGGCGCGCGG | 120 | | | | | | |
| Qy | 185 | CGGGGCGCGACACTGTGGCTGGAGGATGAAAGCGGCTGCCCGACCCCGGCTTTGTTGTT | 244 | | | | | | |
| Db | 121 | TGGGGGTGACACTGTGGCTGGAG-- | 146 | | | | | | |
| Qy | 245 | GCTAATGAGGGAGTGGGCGCAGCGAGCAAGAAAGTGGGTGTACACATCACCTTCAAA | 304 | | | | | | |
| Db | 147 | -----GGGAGTGGGCGCAGCGAGCAAGAAAGTGGGTGTACACATCACCTTCAAA | 198 | | | | | | |
| Qy | 305 | TATGACAAATGTATCACCTACTTGAATCCAGTGGGGAAGCATGTGATTTGCTGACGCCCG | 364 | | | | | | |
| Db | 199 | TATGACAAATGTATCACCTACTTGAATCCAGTGGGGAAGCATGTGATTTGCTGACGCCCG | 258 | | | | | | |
| Qy | 365 | AATATACCAATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCAACATTTCTTTGTCTC | 424 | | | | | | |
| Db | 259 | AATATACCAATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCAACATTTCTTTGTCTC | 318 | | | | | | |
| Qy | 425 | CCAGGGGCGCTCGGCATCGAATTCCTGAAAGGATTTCCGGGTAACTATGAGGAGCTGAAG | 484 | | | | | | |
| Db | 319 | CCAGGGGCGCTCGGCATCGAATTCCTGAAAGGATTTCCGGGTAACTATGAGGAGCTGAAG | 378 | | | | | | |
| Qy | 485 | TCGAGGGAAGACAGTGCACAACTGATTTAAAGGATTCGAAGAGCTCAACAGTAGC | 544 | | | | | | |
| Db | 379 | TCGAGGGAAGACAGTGCACAACTGATTTAAAGGATTCGAAGAGCTCAACAGTAGC | 438 | | | | | | |
| Qy | 545 | TTCAAAAGAACTGAAATGGAACTCAACCTTTCTGAAATATGAAATTTGAAACGGATTAT | 604 | | | | | | |
| Db | 439 | TTCAAAAGAACTGAAATGGAACTCAACCTTTCTGAAATATGAAATTTGAAACGGATTAT | 498 | | | | | | |
| Qy | 605 | TTCTGTAAGGTTGTCCCTTTTCTTCATTTAAATAAGAAAGCAATTAACACCTTTCTTC | 664 | | | | | | |
| Db | 499 | TTCTGTAAGGTTGTCCCTTTTCTTCATTTAAATAAGAAAGCAATTAACACCTTTCTTC | 558 | | | | | | |
| Qy | 665 | TTTAGAACCCGAGCGCTGTGACCTGTGTGTTACAGCGGACAACTATGATTTGTAACCCCTTC | 724 | | | | | | |
| Db | 559 | TTTAGAACCCGAGCGCTGTGACCTGTGTGTTACAGCGGACAACTATGATTTGTAACCCCTTC | 618 | | | | | | |
| Qy | 725 | TGGAAGCGCTCGGAACCTGAAATCAGCGAGCATGGCTCGGACATGCAAGGTGTCCCTCGAC | 784 | | | | | | |
| Db | 619 | TGGAAGCGCTCGGAACCTGAAATCAGCGAGCATGGCTCGGACATGCAAGGTGTCCCTCGAC | 678 | | | | | | |
| Qy | 785 | CATGACCGCAACATTCGGCTTCCTTTCTTCATCTTCACTACAAGCTCAAGCAGAA | 844 | | | | | | |
| Db | 679 | CATGACCGCAACATTCGGCTTCCTTTCTTCATCTTCACTACAAGCTCAAGCAGAA | 738 | | | | | | |
| Qy | 845 | GGACCTTTCAAGCGAAAGACCTGTAAAGCAGGAGCAAACTACAGAGCAGCAGCTGCGCTC | 904 | | | | | | |
| Db | 739 | GGACCTTTCAAGCGAAAGACCTGTAAAGCAGGAGCAAACTACAGAGCAGCAGCTGCGCTC | 798 | | | | | | |
| Qy | 905 | CTTCAAAATGTTTCTCAGGGGATTAATAAATTGAGCTGTGGATGACATAACAACA | 964 | | | | | | |
| Db | 799 | CTTCAAAATGTTTCTCAGGGGATTAATAAATTGAGCTGTGGATGACATAACAACA | 858 | | | | | | |

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|------|----|--|---|------|
| 1939 | Db | | AGCGCCGCTGCAACCCCTGCTGCACACGGTGAAAGCGCGGACGCCCTCGSACATGCGG | 1998 |
| 2105 | Qy | | CGGGACTCAGGCATCTATGACTTGCTGTGTCGCCCTCATCCGAGCTGTCTCTGCCACATGATG | 2164 |
| 1999 | Db | | CGGGACTCAGGCATCTATGACTTGCTGTGTCGCCCTCATCCGAGCTGTCTCTGCCACATGATG | 2058 |
| 2165 | Qy | | GAAGGACTCTCGACGGACCAAGACAGAAACGTCTTCTCTGACGGAGAGCGTGTCTCCTCTCT | 2224 |
| 2059 | Db | | GAAGGACTCTCGACGGACCAAGACAGAAACGTCTTCTCCTGACGGAGAGCGTGTCTCCTCTCT | 2118 |
| 2225 | Qy | | TCAGGCCGTGGTGAGGAGGAACTCTCTGCCCTTCTTCCTCCAGCTCCTCTCTCTCTGGGTCA | 2284 |
| 2119 | Db | | TCAGGCCGTGGTGAGGAGGAACTCTCTGCCCTTCTTCCTTCCAAGTCTCTCTTCTGGGTCA | 2178 |
| 2285 | Qy | | TGCAAGCAGACTTGTGTGTCGCGCAGCTACACTGATGAACTCCACGCGGTGCGCCCTTTTG | 2344 |
| 2179 | Db | | TGCNAAGCAGACTTGTGTGTCGCGCAGCTACACTGATGAACTCCACGCGGTGCGCCCTTTTG | 2238 |
| 2345 | Qy | | TAAACAAACGAAAGAGTCTTAAGCAATTCGCACCTTTAGCTG | 2383 |
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RESULT 14

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US-10-616-788-1
; Sequence 1, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shudian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/39525
; CURRENT APPLICATION NUMBER: US/10/616,788
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 03/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22) .. (2235)
; US-10-616-788-1

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| Db | 199 | TATGACAAATTGTGTACCACTTACTTGAATCCAGTGGGGAAGCATGTGTGATTTGCTGACGCCACG | 258 |
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| Db | 259 | AATATCACCATCAGCCAGTAGTATGCTTGCCATGACCAAGATGGCAGTCAACATTTCTTTGGTGCC | 318 |
| Qy | 425 | CCAGGGCCCTCGGCATCGAAATTTCTGTAAGAGGATTTCCGGTGAATACCTGGAGGAGCTGAAG | 484 |
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| Qy | 485 | TCGGAGGGAAGACAGTGGCCAAACAATGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGGC | 544 |
| Db | 379 | TCGGAGGGAAGACAGTGGCCAAACAATGATTTCTAAAGGATCCGAAGCAGCTCAACAGTAGGC | 438 |
| Qy | 545 | TTCAAAAGAACTCGAAATGGAAATCTCAACCTTTCTCTGAATATGAAATTTTGAAACGGATTTAT | 604 |
| Db | 439 | TTCAAAAGAACTCGAAATGGAAATCTCAACCTTTCTCTGAATATGAAATTTTGAAACGGATTTAT | 498 |
| Qy | 605 | TTCTGTAAGGTTGTTCCTTTTCTCTCCATTAATAAAGAAAGCAATTTACCAACCTTTCTTTC | 664 |
| Db | 499 | TTCTGTAAGGTTGTTCCTTTTCTCTCCATTAATAAAGAAAGCAATTTACCAACCTTTCTTTC | 558 |
| Qy | 665 | TTTATGAACCCGAGCTGTGACCTGTGTGTATACAGCCGACAATCTAGCTTTGTAACCCCTTC | 724 |
| Db | 559 | TTTATGAACCCGAGCTGTGACCTGTGTGTATACAGCCGACAATCTAGCTTTGTAACCCCTTC | 618 |
| Qy | 725 | TGGAAGCCTCGGAACCTGAAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGAC | 784 |
| Db | 619 | TGGAAGCCTCGGAACCTGAAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTTCGAC | 678 |
| Qy | 785 | CATGCACGGCACAACCTTCGGCTTCGGTTTCTTCTATCTTCACTACAGCTCAAGCAGCAA | 844 |
| Db | 679 | CAGCACCGCACAACCTTCGGCTTCGGTTTCTTCTATCTTCACTACAGCTCAAGCAGCAA | 738 |
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| Db | 739 | GGACCTTTCAAGCGAAGAGACTGTAAGCAGGAGCAAACTACAGAGACGACCACTGCTGCCTC | 798 |
| Qy | 905 | CTTCAAAATGTTTCTCCAGGGGATTAATAATTTGAGCTGGTGGATGACATAACACAACA | 964 |
| Db | 799 | CTTCAAAATGTTTCTCCAGGGGATTAATAATTTGAGCTGGTGGATGACATAACACAACA | 858 |
| Qy | 965 | AGAAAAGTGATGCAATTAATGCTTTAAAGCAGTGCATCTCCCGTGGGCGGGCCCATCAGA | 1024 |
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| Qy | 1025 | GCCGTGGCCATCAGTGGCCACTGGTAGTCATATCGSCATTTCCGACGCTTTCACTGTG | 1084 |
| Db | 919 | GCCATGGCCATCAGTGGCCACTGGTAGTCATATCGSCATTTCCGACGCTTTCACTGTG | 978 |
| Qy | 1085 | ATGTGCCGCAAGACCAAGAAAATATATATTTCACTTTAGATGAAGAGAGCTCTGAG | 1144 |
| Db | 979 | ATGTGCCGCAAGACCAAGAAAATATATATTTCACTTTAGATGAAGAGAGCTCTGAG | 1038 |
| Qy | 1145 | TCCTTCCACATACCTGCAGCACTCCCAAGAGAGAGGCTCGGCGCGGGCCGAAGGCTCTTT | 1204 |
| Db | 1039 | TCCTTCCACATACCTGCAGCACTCCCAAGAGAGAGGCTCGGCGCGGGCCGAAGGCTCTTT | 1098 |
| Qy | 1205 | CTCTGCTTTCACAGTAAAGATGGCCGAATCACAATGAATGTCTGTCAGTGTTCGCTTAC | 1264 |
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| Qy | 1265 | TTCTCTCAGGACTTCTCTGGCTGTGAGTGGCTCTGGACCTGTGGGGAAGACTTCAGGCTC | 1324 |
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| Qy | 1325 | TGTAGAGAAGGCGAGAGAAATGGGTCAATCCAGAAGATCCACGAGTCCCAGTTCATCATTT | 1384 |
| Db | 1219 | TGTAGAGAAGGCGAGAGAAATGGGTCAATCCAGAAGATCCACGAGTCCCAGTTCATCATTT | 1278 |
| Qy | 1385 | GTGGTTGTTTCCAAAGGTATGAAGTACTTTGTGACAGAGAGACTACAACACAAAGGA | 1444 |
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QY 1445 GGTGCCGAGCTCGGGAAAGGAGAGCTCTTCTGGTGGCGGTGTACGCAATTCGCGAA 1504
Db 1339 GGTGCCGAGCTCGGGAAAGGAGAGCTCTTCTGGTGGCGGTGTACGCAATTCGCGAA 1398
QY 1505 AAGCTCCGCGAGGCCAAGCAGAGTTCGTCGCGGCGCTCAGCAAGTTTATCGCGTCTAC 1564
Db 1399 AAGCTCCGCGAGGCCAAGCAGAGTTCGTCGCGGCGCTCAGCAAGTTTATCGCGTCTAC 1458
QY 1565 TTGTGATTATCTCTGCGAGGAGAGCTCCCCGATATCTTAGACTGAGTACCAAGTACAGA 1624
Db 1459 TTGTGATTATCTCTGCGAGGAGAGCTCCCCGATATCTTAGACTGAGTACCAAGTACAGA 1518
QY 1625 CTATGGACAATCTCTCAGCTCTGTTCCTCAGCTCCGAGACTCCGAGACCAAGGCTCCAG 1684
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RESULT 15

US-10-842-006-3

; Sequence 3, Application US/10842006

; Publication No. US20040235104A1

; GENERAL INFORMATION:

; APPLICANT: Yang, Ruey-Bing

; TITLE OF INVENTION: A Novel Human SRF Molecule and Uses

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; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MPI03-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)...(2241)
US-10-842-006-3
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Query Match 93.0%; Score 2215.4; DB 20; Length 3083;

Best Local Similarity 97.9%; Pred. No. 0;

Matches 2271; Conservative 0; Mismatches 6; Indels 42; Gaps 1;

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Db 61 GTCAACCCCTCCCTCAACGGCTCCGAGCTGGCTGTGGCCGCTGCGGCTCGGCGCGCG 120
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QY 365 AATATCACCATCAGCAGTATGCTTTGCCATGACCAAGTGGCAGTACCACTCTTTGTGTC 424
Db 259 AATATCACCATCAGCAGTATGCTTTGCCATGACCAAGTGGCAGTACCACTCTTTGTGTC 318
QY 425 CCAGGGGCTTCGGCATGGAATTCCTGAAAGGATTTGGGTAATATCTGGAGAGCTGAAG 484
Db 319 CCAGGGGCTTCGGCATGGAATTCCTGAAAGGATTTGGGTAATATCTGGAGAGCTGAAG 378
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Db 379 TCGAGGGAGACAGTGCACAACTGATTTCTAAAGGATCCGAAAGCAGCTCAACAGTAGC 438
QY 545 TTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACCGAATTAT 604
Db 439 TTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACCGAATTAT 498
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QY 665 TTTAGAACCCGAGCTGTGACCTGTGTTTACAGCCGGAATCTAGCTTTGTAAACCCCTTC 724
Db 559 TTTAGAACCCGAGCTGTGACCTGTGTTTACAGCCGGAATCTAGCTTTGTAAACCCCTTC 618
QY 725 TGGAAAGCTTCGGAACCTGAAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCGAC 784
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QY 785 CATGACCGCACAACTTCGGCTTCGGTTCCTTCTTATCTTCTACTACAGCTCAAGCACGAA 844
Db 679 CACGACCGCACAACTTCGGCTTCGGTTCCTTCTTATCTTCTACTCAAGCTCAAGCACGAA 738
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OM nucleic - nucleic search, using sw model

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(without alignments)
1512.883 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

Total number of hits satisfying chosen parameters: 14611516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 2 | 149 | 100.0 | 2383 | 9 | US-09-912-157-4 |
| 3 | 149 | 100.0 | 2383 | 18 | US-10-717-282-1 |
| 4 | 149 | 100.0 | 2383 | 18 | US-10-717-282-4 |
| 5 | 127 | 85.2 | 2341 | 9 | US-09-912-157-7 |
| 6 | 127 | 85.2 | 2341 | 18 | US-10-717-282-7 |
| 7 | 127 | 85.2 | 4392 | 18 | US-10-343-348-15 |

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| 8 | 127 | 85.2 | 4477 | 20 | US-10-842-006-1 | Sequence 1, Appli |
| 9 | 127 | 85.2 | 4477 | 20 | US-10-608-449-1 | Sequence 1, Appli |
| 10 | 123.8 | 83.1 | 3083 | 9 | US-09-809-567-1 | Sequence 1, Appli |
| 11 | 123.8 | 83.1 | 3083 | 14 | US-10-216-156-1 | Sequence 1, Appli |
| 12 | 123.8 | 83.1 | 3083 | 18 | US-10-616-788-1 | Sequence 3, Appli |
| 13 | 123.8 | 83.1 | 3083 | 20 | US-10-842-006-3 | Sequence 9, Appli |
| 14 | 122.4 | 82.1 | 2786 | 10 | US-09-863-818A-9 | Sequence 9, Appli |
| 15 | 122.4 | 82.1 | 2786 | 19 | US-10-749-144-9 | Sequence 9, Appli |
| 16 | 122.4 | 82.1 | 2786 | 21 | US-10-924-667-9 | Sequence 11, Appli |
| 17 | 122.6 | 75.6 | 2443 | 9 | US-09-912-157-11 | Sequence 11, Appli |
| 18 | 122.6 | 75.6 | 2443 | 18 | US-10-717-282-11 | Sequence 3, Appli |
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| 20 | 104.6 | 70.2 | 2259 | 9 | US-09-912-157-6 | Sequence 3, Appli |
| 21 | 104.6 | 70.2 | 2259 | 18 | US-10-717-282-3 | Sequence 6, Appli |
| 22 | 104.6 | 70.2 | 2259 | 18 | US-10-717-282-6 | Sequence 9, Appli |
| 23 | 88.8 | 59.6 | 2217 | 9 | US-09-912-157-9 | Sequence 9, Appli |
| 24 | 88.8 | 59.6 | 2217 | 18 | US-10-717-282-9 | Sequence 13, Appli |
| 25 | 87.8 | 58.9 | 2217 | 9 | US-09-912-157-13 | Sequence 13, Appli |
| 26 | 87.8 | 58.9 | 2217 | 18 | US-10-717-282-13 | Sequence 12124, A |
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| 28 | 41.6 | 27.9 | 18876 | 16 | US-10-329-079-42 | Sequence 67076, A |
| 29 | 41.6 | 27.9 | 61944 | 16 | US-10-329-079-34 | Sequence 14108, A |
| C 30 | 39.4 | 26.4 | 683 | 19 | US-10-437-963-67076 | Sequence 94316, A |
| C 31 | 38.4 | 25.8 | 567 | 17 | US-10-282-122A-14108 | Sequence 91450, A |
| C 32 | 38 | 25.5 | 460 | 19 | US-10-437-963-94316 | Sequence 92021, A |
| C 33 | 38 | 25.5 | 2196 | 17 | US-10-199-674-4 | Sequence 82999, A |
| C 34 | 37.8 | 25.4 | 666 | 19 | US-10-437-963-91450 | Sequence 156117, A |
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| C 36 | 36.8 | 24.7 | 1305 | 19 | US-10-437-963-82999 | Sequence 55321, A |
| C 37 | 36.6 | 24.6 | 1312 | 20 | US-10-425-115-156117 | Sequence 30778, A |
| C 38 | 36.6 | 24.6 | 1523 | 20 | US-10-739-930-2291 | Sequence 4169, Ap |
| C 39 | 36.6 | 24.6 | 1809 | 20 | US-10-425-115-55321 | Sequence 21360, A |
| C 40 | 36.4 | 24.4 | 506 | 19 | US-10-437-963-30778 | Sequence 76799, A |
| C 41 | 36.2 | 24.3 | 3045 | 19 | US-10-437-963-4169 | Sequence 165870, A |
| C 42 | 36.2 | 24.3 | 4318 | 19 | US-10-437-963-21360 | Sequence 1511, Ap |
| C 43 | 36.2 | 24.3 | 4626 | 19 | US-10-437-963-76799 | |
| C 44 | 36 | 24.2 | 1024 | 20 | US-10-425-115-165870 | |
| C 45 | 35.8 | 24.0 | 555 | 19 | US-10-767-701-1511 | |

ALIGNMENTS

RESULT 1

US-09-912-157-1

Sequence 1, Application US/09912157

Patent No. US20020165348A1

GENERAL INFORMATION:

APPLICANT: Presnell, Scott R.

APPLICANT: Kuestner, Rolf E.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: Human Cytokine Receptor

FILE REFERENCE: 00-49

CURRENT APPLICATION NUMBER: US/09/912,157

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 2383

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (86)...(2344)

US-09-912-157-1

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Best Local Similarity 100.0%; Pred. No. 4.3e-35;

Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 86 ATGGCCCCGTGGTGCAGCTCTGCTCCGCTCTTCTTTACGGTCACCGCTCCCTCAACGGC 145

QY 61 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 120
Db 146 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 205
QY 121 TCGAGGATGAAGCGGCTGCCCGACCCCG 149
Db 206 TCGAGGATGAAGCGGCTGCCCGACCCCG 234

RESULT 2

US-09-912-157-4
; Sequence 4, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
US-09-912-157-4

Query Match 100.0%; Score 149; DB 9; Length 2383;
Best Local Similarity 100.0%; Pred. No. 4.3e-35;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 120
Db 146 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 205
QY 121 TCGAGGATGAAGCGGCTGCCCGACCCCG 149
Db 206 TCGAGGATGAAGCGGCTGCCCGACCCCG 234

RESULT 3

US-10-717-282-1
; Sequence 1, Application US/10717282
; Patent No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)

US-10-717-282-1

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QY 61 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 120
Db 146 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 205
QY 121 TCGAGGATGAAGCGGCTGCCCGACCCCG 149
Db 206 TCGAGGATGAAGCGGCTGCCCGACCCCG 234

RESULT 4

US-10-717-282-4
; Sequence 4, Application US/10717282
; Patent No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
US-10-717-282-4

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Best Local Similarity 100.0%; Pred. No. 4.3e-35;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 120
Db 146 TCGAGCTGGCTGTGGCCGCTGGCGGTCCGGCCCGCGCGGGCGCGACACCTGTGGC 205
QY 121 TCGAGGATGAAGCGGCTGCCCGACCCCG 149
Db 206 TCGAGGATGAAGCGGCTGCCCGACCCCG 234

RESULT 5

US-09-912-157-7
; Sequence 7, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23

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; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2302)
US-09-912-157-7

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Best Local Similarity 93.0%; Pred. No. 1.6e-28;
Matches 133; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      61 TCCAGCTGGCTGTGCCCGCTGGCGGGTCCGGCCGCGCGGGCGCGGACACCTGTGGC 120
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Db      146 TCCAGCTGGCTGTGCCCGCTGGCGGGTCCGGCCGCGCGGGCGCGGACACCTGTGGC 205

Qy      121 TGGAGGATGAAGCGCTGCCCG 143
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Db      206 TGGAGGGAGTGGGGCCAGCCAG 228

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US-10-717-282-7
; Sequence 7, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2302)
US-10-717-282-7

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Best Local Similarity 93.0%; Pred. No. 1.6e-28;
Matches 133; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      121 TGGAGGATGAAGCGCTGCCCG 143
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Db      206 TGGAGGGAGTGGGGCCAGCCAG 228

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US-10-343-348-15
; Sequence 15, Application US/10343348
; Publication No. US20040038242A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Ou, Weijia
; APPLICANT: Su, Eric
; APPLICANT: Tchang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: No. US20040038242A1 secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/10/343,348
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 4392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1662)
; OTHER INFORMATION:
; NAME/KEY: mat peptide
; LOCATION: (82)...( )
; OTHER INFORMATION:
US-10-343-348-15

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Best Local Similarity 93.0%; Pred. No. 1.5e-28;
Matches 133; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy      61 TCCAGCTGGCTGTGCCCGCTGGCGGGTCCGGCCGCGGGCGCGGACACCTGTGGC 120
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Db      61 TCCAGCTGGCTGTGCCCGCTGGCGGGTCCGGCCGCGGGCGCGGACACCTGTGGC 120

Qy      121 TGGAGGATGAAGCGCTGCCCG 143
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Db      121 TGGAGGGAGTGGGGCCAGCCAG 143

RESULT 8
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; Sequence 1, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MPI03-071PIRM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)...(2309)
US-10-842-006-1

Query Match      85.2%; Score 127; DB 20; Length 4477;
Best Local Similarity 93.0%; Pred. No. 1.5e-28;
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RESULT 9
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; Publication No. US20040265834A1
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; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: I2003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-449-1

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RESULT 10
US-09-809-567-1
; Sequence 1, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22) .. (2235)
US-09-809-567-1

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| | Query Match | 83.1% | Score 123.8 | DB 9 | Length 3083 |
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| | Matches 131 | Conservative 0 | Mismatches 12 | Indels 0 | Gaps 0 |
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| Db | 22 | ATGCCCCCGTGGGTGACGCTGCTGCTCGGTCTTTTACGGTCAACGGCTGCCTCAACGGC | 81 | | |
| Qy | 61 | TCGCAGCTGCCTGTGGCCGGCTGGCGGGTCCGGCCGCGCGGGGCGCGCACCTGTGGC | 120 | | |
| Db | 82 | TCGCAGCTGCCTGTGGCCGGCTGGCGGGTCCGGCCGCGCGGTGGGCGTCGACACCTGTGGC | 141 | | |
| Qy | 121 | TGGAGGATGAAGCGGCTGCCCG | 143 | | |
| Db | 142 | TGGAGGGAGTGGGGCCAGGCAG | 164 | | |

RESULT 11
 US-10-216-156-1
 ; Sequence 1, Application US/10216156
 ; Publication No. US2003009980A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jing Shuqian
 ; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
 ; FILE REFERENCE: 01017/36916A
 ; CURRENT APPLICATION NUMBER: US/10/216,156
 ; CURRENT FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: US/09/809,567
 ; PRIOR FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: 09/724,460
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 60/189,816
 ; PRIOR FILING DATE: 2000-03-16
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 ; SOFTWARE: PatentIn Ver. 2.0
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 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (22)..(2235)
 ; US-10-216-156-1

RESULT 12
US-10-616-788-1
Sequence 1, Application US/10616788
Publication No. US20040048338A1
GENERAL INFORMATION:
Applicant: Jing. Shuqian
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
FILE REFERENCE: 01017/39525
CURRENT APPLICATION NUMBER: US/10/616,788
CURRENT FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: 09/809,567
PRIOR FILING DATE: 2001-03-15

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:40:52 ; Search time 109.034 Seconds
(without alignments)
2696.128 Million cell updates/sec

Title: US-10-717-282-2

Perfect score: 4013

Sequence: 1 MAPWLQCSVFTVNAACLG.....CKADLGCRSYDELHVAAPL 753

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
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| 2 | 4013 | 100.0 | 753 | Sequence 2, Appli |
| 3 | 4003 | 99.8 | 753 | US-10-717-282-2 |
| 4 | 4003 | 99.8 | 753 | Sequence 5, Appli |
| 5 | 3925 | 97.8 | 739 | US-10-717-282-5 |
| 6 | 3925 | 97.8 | 739 | Sequence 8, Appli |
| 7 | 3915 | 97.6 | 739 | US-10-717-282-8 |
| 8 | 3915 | 97.6 | 739 | Sequence 2, Appli |
| 9 | 3905 | 97.3 | 739 | US-10-842-006-2 |
| 10 | 3901 | 97.2 | 738 | US-10-842-006-4 |
| 11 | 3901 | 97.2 | 738 | US-09-809-567-2 |

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| 12 | 3901 | 97.2 | 738 | 15 | US-10-616-788-2 | Sequence 2, Appli |
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| 14 | 3835.5 | 95.6 | 738 | 16 | US-10-749-144-10 | Sequence 10, Appl |
| 15 | 3835.5 | 95.6 | 738 | 17 | US-10-924-667-10 | Sequence 10, Appl |
| 16 | 3708 | 92.6 | 728 | 15 | US-10-104-047-3399 | Sequence 3399, Ap |
| 17 | 3703 | 92.3 | 728 | 9 | US-09-874-503-18 | Sequence 18, Appl |
| 18 | 3703 | 92.3 | 728 | 10 | US-09-816-744-18 | Sequence 18, Appl |
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| 20 | 3703 | 92.3 | 728 | 10 | US-09-908-827-18 | Sequence 18, Appl |
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| 22 | 3703 | 92.3 | 728 | 14 | US-10-410-927-18 | Sequence 18, Appl |
| 23 | 3703 | 92.3 | 728 | 14 | US-10-410-374-18 | Sequence 18, Appl |
| 24 | 3703 | 92.3 | 728 | 14 | US-10-410-552-18 | Sequence 18, Appl |
| 25 | 3703 | 92.3 | 728 | 15 | US-10-458-442-18 | Sequence 18, Appl |
| 26 | 3703 | 92.3 | 728 | 15 | US-10-408-385-18 | Sequence 18, Appl |
| 27 | 3387 | 84.4 | 739 | 9 | US-09-912-157-12 | Sequence 12, Appl |
| 28 | 3387 | 84.4 | 739 | 15 | US-10-717-282-12 | Sequence 12, Appl |
| 29 | 3176 | 79.1 | 595 | 17 | US-10-477-714-16 | Sequence 16, Appl |
| 30 | 3170 | 79.0 | 595 | 16 | US-10-608-449-4 | Sequence 4, Appli |
| 31 | 2699.5 | 67.3 | 554 | 15 | US-10-343-348-16 | Sequence 16, Appl |
| 32 | 1337 | 33.3 | 296 | 15 | US-10-616-788-19 | Sequence 19, Appl |
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| 35 | 312 | 7.8 | 810 | 15 | US-10-616-788-3 | Sequence 3, Appli |
| 36 | 312 | 7.8 | 866 | 9 | US-09-778-971-9 | Sequence 9, Appli |
| 37 | 312 | 7.8 | 866 | 13 | US-10-033-522-1 | Sequence 1, Appli |
| 38 | 312 | 7.8 | 866 | 14 | US-10-207-655-107 | Sequence 107, App |
| 39 | 312 | 7.8 | 866 | 16 | US-10-742-161-10 | Sequence 10, Appl |
| 40 | 312 | 7.8 | 866 | 16 | US-10-742-372-10 | Sequence 10, Appl |
| 41 | 312 | 7.8 | 866 | 16 | US-10-646-308-4 | Sequence 4, Appli |
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| 44 | 306 | 7.6 | 864 | 16 | US-10-742-372-2 | Sequence 2, Appli |
| 45 | 232.5 | 5.8 | 207 | 10 | US-09-863-818A-19 | Sequence 19, Appl |

ALIGNMENTS

RESULT 1
US-09-912-157-2
; Sequence 2, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-2

Query Match 100.0%; Score 4013; DB 9; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 753; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 2, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-282-2
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Best Local Similarity 100.0%; Pred. No. 0;
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; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-5
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US-10-717-282-5

; Sequence 5, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-717-282-5
Query Match 99.8%; Score 4003; DB 15; Length 753;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 MAPLQLCSVFTVNACLSQSLAAAGSGRARGADTCGRMKAAARPRLCVANEGVGP 60
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Db 61 ASRNSGLNYITFKYDNCCTTYLNPVKGKVIADAQNTTISQYACHDOVAVTILWSPGALGIE 120
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Db 721 PPALPSKLLSSGCKADLGCRTSYTDELHAAVPL 753

RESULT 5

US-09-912-157-8

; Sequence 8, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0

Sat Aug 13 10:40:54 2005

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; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-8

Query Match      97.8%; Score 3925; DB 9; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

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Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 646

Qy 661 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 720
Db 647 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 706

Qy 721 PPALPSKLLSSGCKADLGCRSYTDELHAVAPL 753
Db 707 PPALPSKLLSSGCKADLGCRSYTDELHAVAPL 739
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RESULT 6
US-10-717-282-8
; Sequence 8, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
```

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; CURRENT APPLICATION NUMBER: US/10717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-282-8
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Query Match      97.8%; Score 3925; DB 15; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFFTVNACINGSQLAAGAAGSGRAGADTCGWRKMAAARPRCLCVANEVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLAAGAAGSGRAGADTCGWR-----GVGP 46

Qy 61 ASRNSGLYNTTFKYDNCCTTYLNPVGKHVIAADAQNTTISQYACHDOQAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTTFKYDNCCTTYLNPVGKHVIAADAQNTTISQYACHDOQAVTILWSPGALGIE 106

Qy 121 FLKGFVILBELKSEGRQCOQLILKDPKQLNSSFKRTGMESQPFLLMKFETDYFVKVVPF 180
Db 107 FLKGFVILBELKSEGRQCOQLILKDPKQLNSSFKRTGMESQPFLLMKFETDYFVKVVPF 166

Qy 181 PSIKNESNYHFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 240
Db 167 PSIKNESNYHFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHNFG 226

Qy 241 FRFFYLHYKLKHEGPFKRTCKQBOETTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 227 FRFFYLHYKLKHEGPFKRTCKQBOETTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSSTYTAA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 480
Db 407 WVIQKHESQFIIVVCSKGMKYFVDKKNYKHGGSGRGKGEFLVAVSAIAEKLROAKQ 466

Qy 481 SSSAALSXFIAYFDYSCGDPVGLDLSLTKYRLMDNLPLQCSHLHSDHGLQSPGOHTR 540
Db 467 SSSAALSXFIAYFDYSCGDPVGLDLSLTKYRLMDNLPLQCSHLHSDHGLQSPGOHTR 526

Qy 541 QGSRNRYFRSKGRSLYVAICNMHQFIDEEDPDWFEKQFVPPHPPPLRYREPVLKFDPSGL 600
Db 527 QGSRNRYFRSKGRSLYVAICNMHQFIDEEDPDWFEKQFVPPHPPPLRYREPVLKFDPSGL 586

Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHSQHGGLDQGEARPALDGSAAALQPL 646

Qy 661 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 720
Db 647 LHTVKAGSPDMPRDSGIYDSSVSPSSLSPLMEGLSTDQETSSLTESVSSSGLGEE 706

Qy 721 PPALPSKLLSSGCKADLGCRSYTDELHAVAPL 753
Db 707 PPALPSKLLSSGCKADLGCRSYTDELHAVAPL 739
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RESULT 7
US-10-842-006-2
; Sequence 2, Application US/10842006
; Publication No. US20040235104A1
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Sat Aug 13 10:40:54 2005

GENERAL INFORMATION:

APPLICANT: Yang, Ruy-Bing
TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
FILE REFERENCE: MP103-071PIRM
CURRENT APPLICATION NUMBER: US/10/842,006
PRIOR FILING DATE: 2004-05-07
CURRENT FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 739
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-842-006-2

Query Match 97.6%; Score 3915; DB 16; Length 739;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEGVGP 46
61 ASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQVACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQVACHDQVAVTILWSPGALGIE 106
Qy 121 FLKGRFVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 180
Db 107 FLKGRFVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 166
Qy 181 PSIKNESNYHPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 240
Db 167 PSIKNESNYHPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 226
Qy 241 FRPFYLYKLKHEGPFKRKTCQEQTTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 300
Db 227 FRPFYLYKLKHEGPFKRKTCQEQTTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 286
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346
Qy 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406
Qy 421 WVIQKIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 480
Db 407 WVIQKIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 466
Qy 481 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 540
Db 467 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 526
Qy 541 QGSRNNYFRSKGSLYVAICNMHQFIDEEPDPWEKQVPPHPPPLRYRPPVLEKFDGSL 600
Db 527 QGSRNNYFRSKGSLYVAICNMHQFIDEEPDPWEKQVPPHPPPLRYRPPVLEKFDGSL 586
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 646
Qy 661 LHTVKGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTSESVSSSSGLGEE 720
Db 647 LHTVKGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTSESVSSSSGLGEE 706
721 PPALPSKLLSSGCKADIGCRSYTDELHAVAPL 753
707 PPALPSKLLSSGCKADIGCRSYTDELHAVAPL 739

RESULT 8

US-10-608-449-2
Sequence 2, Application US/10608449
Publication No. US20040265834A1
GENERAL INFORMATION:
APPLICANT: Tsinghua University
TITLE OF INVENTION: Human interleukin-17 Receptor Like Molecule
FILE REFERENCE: I2003269C-US
CURRENT APPLICATION NUMBER: US/10/608,449
CURRENT FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 739
TYPE: PRT
ORGANISM: Homo sapiens
US-10-608-449-2

Query Match 97.6%; Score 3915; DB 16; Length 739;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLA VAAAGSGRARGADTCGRMKAAARPRLCVANEGVGP 46
61 ASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQVACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTFFKYDNCCTTYLNPVGKHVIADAQNITISQVACHDQVAVTILWSPGALGIE 106
Qy 121 FLKGRFVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 180
Db 107 FLKGRFVILELSEKSGRQCQQLILKDPKQLNSSFKRTGMESQPLNMFETDYFVKVVPF 166
Qy 181 PSIKNESNYHPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 240
Db 167 PSIKNESNYHPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 226
Qy 241 FRPFYLYKLKHEGPFKRKTCQEQTTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 300
Db 227 FRPFYLYKLKHEGPFKRKTCQEQTTETTSCLLQNVSPGDYIILELVDNTTTRKVMHYA 286
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346
Qy 361 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKQGNHNVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406
Qy 421 WVIQKIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 480
Db 407 WVIQKIHESQPIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAQK 466
Qy 481 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 540
Db 467 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 526
Qy 541 QGSRNNYFRSKGSLYVAICNMHQFIDEEPDPWEKQVPPHPPPLRYRPPVLEKFDGSL 600
Db 527 QGSRNNYFRSKGSLYVAICNMHQFIDEEPDPWEKQVPPHPPPLRYRPPVLEKFDGSL 586
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAQPL 646
Qy 661 LHTVKGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTSESVSSSSGLGEE 720
Db 647 LHTVKGSPSDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSSLTSESVSSSSGLGEE 706
721 PPALPSKLLSSGCKADIGCRSYTDELHAVAPL 753

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Db 707 PPALPSKLLSSGCKADLGRSYTDELHAVAPL 739
RESULT 9
US-10-842-006-4
; Sequence 4, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruy-Bing
; TITLE OF INVENTION: A Novel Human SEP Molecule and Uses
; FILE OF INVENTION: Therefor
; FILE REFERENCE: MPI03-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842.006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-4

Query Match 97.3%; Score 3905; DB 16; Length 739;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 735; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFFTVNACINGSQLAVAAGGSRGARGADTCGRMKAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLAVAAGGSRGARGADTCGRMKAAARPRLCVANEGVGP 46

Qy 61 ASRNSGLYNITFKYDNCCTTYLNPVKHVIADAQNITISQYACHDOVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNITFKYDNCCTTYLNPVKHVIADAQNITISQYACHDOVAVTILWSPGALGIE 106

Qy 121 FLKGFVRILELSEKRGQCQQLIKDPKQLNSSFKRTGMESQPLNKKFETDYFVKVVPF 180
Db 107 FLKGFVRILELSEKRGQCQQLIKDPKQLNSSFKRTGMESQPLNKKFETDYFVKVVPF 166

Qy 181 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 240
Db 167 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 226

Qy 241 FRFYLHYKLKHEGPFKRKTKQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300
Db 227 FRFYLHYKLKHEGPFKRKTKQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQNHMVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQNHMVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAISAIAEKLRAQK 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAISAIAEKLRAQK 466

Qy 481 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 540
Db 467 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 526

Qy 541 QGSRNRNFRSKSGSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYREPVLEKFDGSL 600
Db 527 QGSRNRNFRSKSGSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYREPVLEKFDGSL 586

Qy 601 VLNDVMCKPGPESDFCLKVEAVLIGATGPADSOHESQHGGLDODGEARPALDGSAAQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAVLIGATGPADSOHESQHGGLDODGEARPALDGSAAQPL 646

Qy 661 LHTVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTETSSLSVSSSSGLGEE 720
Db 647 LHTVKAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTETSSLSVSSSSGLGEE 706

RESULT 10
US-09-809-567-2
; Sequence 2, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shugian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-567-2

Query Match 97.2%; Score 3901; DB 9; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFFTVNACINGSQLAVAAGGSRGARGADTCGRMKAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFFTVNACINGSQLAVAAGGSRGARGADTCGRMKAAARPRLCVANEGVGP 46

Qy 61 ASRNSGLYNITFKYDNCCTTYLNPVKHVIADAQNITISQYACHDOVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNITFKYDNCCTTYLNPVKHVIADAQNITISQYACHDOVAVTILWSPGALGIE 106

Qy 121 FLKGFVRILELSEKRGQCQQLIKDPKQLNSSFKRTGMESQPLNKKFETDYFVKVVPF 180
Db 107 FLKGFVRILELSEKRGQCQQLIKDPKQLNSSFKRTGMESQPLNKKFETDYFVKVVPF 166

Qy 181 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 240
Db 167 PSIKNESNYHPFFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPNFG 226

Qy 241 FRFYLHYKLKHEGPFKRKTKQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300
Db 227 FRFYLHYKLKHEGPFKRKTKQEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 286

Qy 301 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346
Db 287 LKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAA 346

Qy 361 LPRERLRPRPKVFLCYSSKDGQNHMVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRPKVFLCYSSKDGQNHMVVQCFAFLQDFCGCEVALDLWEDFSLCREGORE 406

Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAISAIAEKLRAQK 480
Db 407 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAISAIAEKLRAQK 466

Qy 481 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 540
Db 467 SSSAALSXFIAYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQBPQGHTR 526

Qy 541 QGSRNRNFRSKSGSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYREPVLEKFDGSL 600
Db 527 QGSRNRNFRSKSGSLYVAICNMHQFIDEEPWFKEQFVPPHPPPLRYREPVLEKFDGSL 586
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Qy 601 VLVDMCKPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAALQPL 660
Db 587 VLVDMCKPESDFCLKVEAPVLGATGPADSOHESQHGGLDQDGEARPALDGSAAALQPL 646
Qy 661 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSSLSSESGLGEE 720
Db 647 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSSLSSESGLGEE 706
Qy 721 PPALPSKLLSSGCKADLGCERSYTDHNAVAP 752
Db 707 PPALPSKLLSSGCKADLGCERSYTDHNAVAP 738
RESULT 11
US-10-216-156-2
; Sequence 2, Application US/10216156
; Publication No. US2003009980A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-156-2
Query Match 97.2%; Score 3901; DB 14; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFTVYVACNGSLQAVAGSGRARGADTCGWRMKAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFTVYVACNGSLQAVAGSGRARGADTCGWRMKAARPRLCVANEGVGP 46
Qy 61 ASRNSGLYNTTFKYDNCNTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTTFKYDNCNTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 106
Qy 121 FLKGRVILELKSREGCOQILKDPKQLNSSFKRTGMSQPPFLNMKFETDYFKVVPF 180
Db 107 FLKGRVILELKSREGCOQILKDPKQLNSSFKRTGMSQPPFLNMKFETDYFKVVPF 166
Qy 181 PSIKNESYHPPFTRACDILLODNLACPKFWMKPRNLINSQHGSDMQVSDHAPHNFG 240
Db 167 PSIKNESYHPPFTRACDILLODNLACPKFWMKPRNLINSQHGSDMQVSDHAPHNFG 226
Qy 241 FRFFYLHYKLKHEGPFKRTCKEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 227 FRFFYLHYKLKHEGPFKRTCKEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDEESESSTYTA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDEESESSTYTA 346
Qy 361 LPRERLRPRKPVFLCYSSKOGQNHVNVQCFAIFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRERLRPRKPVFLCYSSKOGQNHVNVQCFAIFLQDFCGCEVALDLWEDFSLCREGORE 406
Qy 421 WVIQIHESQFTIIVCCKGMKVFVDKQYKHGGRGSGKGBELFLVAVSAEKLRAQK 480
Db 407 WVIQIHESQFTIIVCCKGMKVFVDKQYKHGGRGSGKGBELFLVAVSAEKLRAQK 466

Qy 481 SSSAALSKFIAVVPDYSCEGDVPGIILDLSTKYRLMDNLPOLCSHLHSRDHGLQBPQGHTR 540
Db 467 SSSAALSKFIAVVPDYSCEGDVPGIILDLSTKYRLMDNLPOLCSHLHSRDHGLQBPQGHTR 526
Qy 541 QGSRNRYFRKSGRSLVAICNMHQFIDEBPDWFEKQFVPHPPPLAYRREPVLEKFDGSL 600
Db 527 QGSRNRYFRKSGRSLVAICNMHQFIDEBPDWFEKQFVPHPPPLAYRREPVLEKFDGSL 586
Qy 601 VLVDMCKPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAAALQPL 660
Db 587 VLVDMCKPESDFCLKVEAPVLGATGPADSOHESQHGGLDQDGEARPALDGSAAALQPL 646
Qy 661 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSSLSSESGLGEE 720
Db 647 LHTVAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTTSTSSLSSESGLGEE 706
Qy 721 PPALPSKLLSSGCKADLGCERSYTDHNAVAP 752
Db 707 PPALPSKLLSSGCKADLGCERSYTDHNAVAP 738
RESULT 12
US-10-616-788-2
; Sequence 2, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/39525
; CURRENT APPLICATION NUMBER: US/10/616,788
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-788-2
Query Match 97.2%; Score 3901; DB 15; Length 738;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;
Qy 1 MAPWLQCSVFTVYVACNGSLQAVAGSGRARGADTCGWRMKAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFTVYVACNGSLQAVAGSGRARGADTCGWRMKAARPRLCVANEGVGP 46
Qy 61 ASRNSGLYNTTFKYDNCNTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTTFKYDNCNTTYLNPVKGKVIADAQNTTISQYACHDQVAVTILWSPGALGIE 106
Qy 121 FLKGRVILELKSREGCOQILKDPKQLNSSFKRTGMSQPPFLNMKFETDYFKVVPF 180
Db 107 FLKGRVILELKSREGCOQILKDPKQLNSSFKRTGMSQPPFLNMKFETDYFKVVPF 166
Qy 181 PSIKNESYHPPFTRACDILLODNLACPKFWMKPRNLINSQHGSDMQVSDHAPHNFG 240
Db 167 PSIKNESYHPPFTRACDILLODNLACPKFWMKPRNLINSQHGSDMQVSDHAPHNFG 226
Qy 241 FRFFYLHYKLKHEGPFKRTCKEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 300
Db 227 FRFFYLHYKLKHEGPFKRTCKEQTTTSCLLQNVSPGDYIIELVDDTNTTRKVMHYA 286
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDEESESSTYTA 360
Db 287 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQOENIYSHLDEESESSTYTA 346

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Qy 361 LPRRLRPRPKVFLCYSSKDGQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 347 LPRRLRPRPKVFLCYSSKDGQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 406
Qy 421 WVIQIHESQFIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAKQ 480
Db 407 WVIQIHESQFIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAKQ 466
Qy 481 SSSAALSFTAVFYDSCGDPVGLDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
Db 467 SSSAALSFTAVFYDSCGDPVGLDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 526
Qy 541 QGSRNRYFRSKGSLVVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRPPVLEKFPDGL 600
Db 527 QGSRNRYFRSKGSLVVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRPPVLEKFPDGL 586
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATCPADSQHESQHGGGLDQDGEARPALDGSAAALQPL 660
Db 587 VLNDVMCKPGPESDFCLKVEAAVLGATCPADSQHESQHGGGLDQDGEARPALDGSAAALQPL 646
Qy 661 LHTVKAGSPDMPRDSGIYDSSVSPSELPLMEGLSTDQTTSSLTSSVSSSGLGEE 720
Db 647 LHTVKAGSPDMPRDSGIYDSSVSPSELPLMEGLSTDQTTSSLTSSVSSSGLGEE 706
Qy 721 PPALPSKLLSSGCKADLGCRSYTDELHVAAP 752
Db 707 PPALPSKLLSSGCKADLGCRSYTDELHVAAP 738

RESULT 13
US-09-863-818A-10
; Sequence 10, Application US/09863818A
; Publication No. US20030092881A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/09/863,818A
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18)..(19)
; OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
; NAME/KEY: misc feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
; NAME/KEY: misc feature
; LOCATION: (120)..(120)
; OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
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; NAME/KEY: misc feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; NAME/KEY: misc feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-09-863-818A-10
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Query Match 95.6%; Score 3835.5; DB 10; Length 738;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;

Qy 1 MAPWLQLCVFFFTVNACLSQLAVAAGSGRARGADTCGRMKAAARPRLCVANEGVGP 60
Db 1 MAPWLQLCVFFFTVNACLSQLAVAAGSGRARGADTCG-----XGVGP 46
Qy 61 ASRNSGLYNTTFKYDNCCTTYLNPVGHVIAADAQNITISQYACHDOVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTTFKYDNCCTTYLNPVGHVIAADAQNITISQYACHDOVAVTILWSPGALGIE 106
Qy 121 FLKGRFVILEELKSEGRQCOOLILKDPKQLNSSFKRTGMESQPLNKKMFETDYFKVVPF 180
Db 107 FLKGRFVILEELKSEGRQXOOLILKDPKQXNSSFKRTGMESQPLNKKMFETDYFVR-LSP 165
Qy 181 PSIKNESNYHPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVVSFDHAPNFG 240
Db 166 SFIKNESNYHPFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVVSFDHAPNFG 225
Qy 241 FRFFYLHYKLKHEGPPFRKTKCOEOTTETTSCLLQNVSPGDYIELVDDNTTRKVMHYA 300
Db 226 FRFFYLHYKLKHEGPPFRKTKCOEOTTETTSCLLQNVSPGDYIELVDDNTTRKVMHYA 285
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTWCKRKKQENIYSHLDESSSESTYTA 360
Db 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTWCKRKKQENIYSHLDESSSESTYTA 345
Qy 361 LPRRLRPRPKVFLCYSSKDGQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 346 LPRRLRPRPKVFLCYSSKDGQGNHNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 405
Qy 421 WVIQIHESQFIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAKQ 480
Db 406 WVIQIHESQFIIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLRAKQ 465
Qy 481 SSSAALSFTAVFYDSCGDPVGLDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 540
Db 466 SSSAALSFTAVFYDSCGDPVGLDLSTKYRLMDNLPQLCSHLHSRDHGLQEPGQHTR 525
Qy 541 QGSRNRYFRSKGSLVVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRPPVLEKFPDGL 600
Db 526 QGSRNRYFRSKGSLVVAICNMHQFIDEBPDWFEKQFVPPHPPPLRYRPPVLEKFPDGL 585
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATCPADSQHESQHGGGLDQDGEARPALDGSAAALQPL 660
Db 586 VLNDVMCKPGPESDFCLKVEAAVLGATCPADSQHESQHGGGLDQDGEARPALDGSAAALQPL 645
Qy 661 LHTVKAGSPDMPRDSGIYDSSVSPSELPLMEGLSTDQTTSSLTSSVSSSGLGEE 720
Db 646 LHTVKAGSPDMPRDSGIYDSSVSPSELPLMEGLSTDQTTSSLTSSVSSSGLGEE 705
Qy 721 PPALPSKLLSSGCKADLGCRSYTDELHVAAPL 753
Db 706 PPALPSKLLSSGCKADLGCRSYTDELHVAAPL 738
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RESULT 14
US-10-749-144-10


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; Sequence 10, Application US/10749144
; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; CURRENT FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120)..(120)
; OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
; -10-749-144-10
Query Match          95.6%; Score 3835.5; DB 16; Length 738;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;
Qy 1 MAPWLQCSVFTVNAACGLSGLVAAGSGRARGADTCGRMKAAARPRLCVANEVGVP 60
Db 1 MAPWLQCSVFTVNAACGLSGLVAAGSGRARGADTCGRMKAAARPRLCVANEVGVP 60
Qy 61 ASRNSGLNITFKYDNCNTYLNPKGVHVIADQAQNTISQYACHDOVAVTILWSPGALGIE 120
Db 61 ASRNSGLNITFKYDNCNTYLNPKGVHVIADQAQNTISQYACHDOVAVTILWSPGALGIE 120
Qy 121 FLKGRVILELKGEGROCOQLILKDPKOLNSSFKRTGMSQPLNLMKFETDIFVKVVPF 180
Db 121 FLKGRVILELKGEGROCOQLILKDPKOLNSSFKRTGMSQPLNLMKFETDIFVKVVPF 180
Qy 107 FLKGRVILELKGEGROCOQLILKDPKOLNSSFKRTGMSQPLNLMKFETDIFVR-USF 165
Db 107 FLKGRVILELKGEGROCOQLILKDPKOLNSSFKRTGMSQPLNLMKFETDIFVR-USF 165
Qy 181 PSIKESNYHPFFTRACDILLOPDNLACPKFPWKPRNLINISQHGSDMQVDFDHPHNF 240
Db 181 PSIKESNYHPFFTRACDILLOPDNLACPKFPWKPRNLINISQHGSDMQVDFDHPHNF 240
Qy 166 SFIKESNYHPFFTRACDILLOPDNLACPKFPWKPRNLINISQHGSDMQVDFDHPHNF 225
Db 166 SFIKESNYHPFFTRACDILLOPDNLACPKFPWKPRNLINISQHGSDMQVDFDHPHNF 225
Qy 241 FRFFYLHYLKHGEPFKRTCKEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300
Db 241 FRFFYLHYLKHGEPFKRTCKEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300
Qy 256 FRFFYLHYLKHGEPFKRTCKEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 285
Db 256 FRFFYLHYLKHGEPFKRTCKEQTTTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 285
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQENIYSHLDEESSESTYTA 360
Db 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQENIYSHLDEESSESTYTA 360
Qy 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQENIYSHLDEESSESTYTA 345
Db 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQENIYSHLDEESSESTYTA 345
Qy 361 LPRRLRPKPVFLCVSSKDGQNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 361 LPRRLRPKPVFLCVSSKDGQNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Qy 346 LPRRLRPKPVFLCVSSKDGQNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 405
Db 346 LPRRLRPKPVFLCVSSKDGQNNVQCFAYFLQDFCGCEVALDLWEDFSLCREGORE 405
Qy 421 WVIQIHESQFIIVVCSKGMKYFVDKQNYKHGGGSGKGLFLVAVSAIAEKLRQAKQ 480
Db 421 WVIQIHESQFIIVVCSKGMKYFVDKQNYKHGGGSGKGLFLVAVSAIAEKLRQAKQ 480
Qy 406 WVIQIHESQFIIVVCSKGMKYFVDKQNYKHGGGSGKGLFLVAVSAIAEKLRQAKQ 465
Db 406 WVIQIHESQFIIVVCSKGMKYFVDKQNYKHGGGSGKGLFLVAVSAIAEKLRQAKQ 465
Qy 481 SSSAALSFKFIAYFDYSCGEGVPGIILDLSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540
Db 481 SSSAALSFKFIAYFDYSCGEGVPGIILDLSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540
Qy 466 SSSAALSFKFIAYFDYSCGEGVPGIILDLSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 525
Db 466 SSSAALSFKFIAYFDYSCGEGVPGIILDLSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 525
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Db 541 QGSRNRYFRSKSGRSLYVAICNMHOFIDEEPWFEEKOFVPPHPPPLRYREPVLKFDGSL 600
Qy 526 QGSRNRYFRSKSGRSLYVAICNMHOFIDEEPWFEEKOFVPPHPPPLRYREPVLKFDGSL 585
Db 526 QGSRNRYFRSKSGRSLYVAICNMHOFIDEEPWFEEKOFVPPHPPPLRYREPVLKFDGSL 585
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGGLDQDGEARPALDGSAAALQPL 660
Db 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGGLDQDGEARPALDGSAAALQPL 660
Qy 586 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGGLDQDGEARPALDGSAAALQPL 645
Db 586 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGGLDQDGEARPALDGSAAALQPL 645
Qy 661 LHTVAGSPDMPRDSGIYSSVSPSSLSLPLMGLSTDQTTSTSTSTSTSTSTSTSTSTSTST 720
Db 661 LHTVAGSPDMPRDSGIYSSVSPSSLSLPLMGLSTDQTTSTSTSTSTSTSTSTSTSTSTST 720
Qy 646 LHTVAGSPDMPRDSGIYSSVSPSSLSLPLMGLSTDQTTSTSTSTSTSTSTSTSTSTSTST 705
Db 646 LHTVAGSPDMPRDSGIYSSVSPSSLSLPLMGLSTDQTTSTSTSTSTSTSTSTSTSTSTST 705
Qy 721 PPALPSKLLSGSGCKADLGCESYTDLHVAAPL 753
Db 721 PPALPSKLLSGSGCKADLGCESYTDLHVAAPL 753
Qy 706 PPALPSKLLSGSGCKADLGCESYTDLHVAAPL 738
Db 706 PPALPSKLLSGSGCKADLGCESYTDLHVAAPL 738
RESULT 15
US-10-924-667-10
; Sequence 10, Application US/10924667
; Publication No. US20050009145A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: DX01170K
; CURRENT APPLICATION NUMBER: US/10/924,667
; CURRENT FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: US/09/863,818
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/206,862
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (18)..(18)
; OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or
; OTHER INFORMATION: Met.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)..(26)
; OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or
; OTHER INFORMATION: Met.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109)..(109)
; OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or
; OTHER INFORMATION: Cys.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120)..(120)
; OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or
; OTHER INFORMATION: Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (134)..(134)
; OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (144)..(144)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (170)..(170)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (475)..(475)
; OTHER INFORMATION: unknown amino
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (519)..(519)
; OTHER INFORMATION: unknown amino
US-10-924-667-10

Query Match 95.6%; Score 3835.5; DB 17; Length 738;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 726; Conservative 2; Mismatches 10; Indels 15; Gaps 2;
Qy 1 MAPWLQCSVFFVTNACLSQLAAGAAGSGRARGADTCGRWMAAARPRLCVANEGVGP 60
Db 1 MAPWLQCSVFFVTNACLSQLAAGAAGSGRARGADTCW-----XGVGP 46
Qy 61 ASRNSGLYNTFFKYNCTTYLNPVKHVIADAQNITTSYACHDQVAVTILWSPGALGIE 120
Db 47 ASRNSGLYNTFFKYNCTTYLNPVKHVIADAQNITTSYACHDQVAVTILWSPGALGIE 106
Qy 121 FLKGFVILELSEKQCOOLILKDPKOLNSSFKRTGMESQPLNMKFETDYEVKVVVF 180
Db 107 FLKGFVILELSEKQCOOLILKDPKOLNSSFKRTGMESQPLNMKFETDYFVR-LSF 165
Qy 181 PSIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 240
Db 166 SFIKNESNYHPPFRTRACDILLQPDNLACKPFWKPRNLNISQHGSDMQVSDHAPHNFG 225
Qy 241 FRPFLHYKLKHEGPFKRTCKQQTETTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 300
Db 226 FRPFLHYKLKHEGPFKRTCKQQTETMTSCLLQNVSPGDIYIELVDDTNTTRKVMHYA 285
Qy 301 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQQENIYSHLDESSSSTYTA 360
Db 286 LKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKQQENIYSHLDESSSSTYTA 345
Qy 361 LPRRLRPRPKVFLCYSSKQGNHNVVQCFCAYFLQDFCGCEVALDLWEDFSLCREGORE 420
Db 346 LPRRLRPRPKVFLCYSSKQGNHNVVQCFCAYFLQDFCGCEVALDLWEDFSLCREGORE 405
Qy 421 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLROAKQ 480
Db 406 WVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGSGKGELFLVAVSAIAEKLROAKQ 465
Qy 481 SSSAALSKFIANYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 540
Db 466 SSSAALSKFIANYFDYSCGDPVGLDLSTKYRLMDNLPLQCSHLHSDHGLQEPGQHTR 525
Qy 541 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPDWFEKQFVPHPPPLRYREPVLKFDGSL 600
Db 526 QGSRNRYFRSKGRSLYVAICNMHQFIDEEPDWFEKQFVPHPPPLRYREPVLKFDGSL 585
Qy 601 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAALOPL 660
Db 586 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSOHESQHGGLDQDGEARPALDGSAALOPL 645
Qy 661 LHTVKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 720

Db 646 LHTVKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQTETSSLTESVSSSGLGEEE 705
Qy 721 PPALPSKLLSSGSKADLGCRSYTDELHVAAPL 753
Db 706 PPALPSKLLSSGSKADLGCRSYTDELHVAAPL 738
Search completed: August 9, 2005, 11:54:38
Job time : 112.034 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 9, 2005, 11:40:52 ; Search time 103.966 Seconds
(without alignments)
2696.128 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGWRKAAARPRCLVAN.....CKADLGRSYDELHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 39037842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------|
| 1 | 3829 | 100.0 | 753 | 9 | US-09-912-157-2 |
| 2 | 3829 | 100.0 | 753 | 15 | US-10-717-282-2 |
| 3 | 3819 | 99.7 | 753 | 9 | US-09-912-157-5 |
| 4 | 3819 | 99.7 | 753 | 15 | US-10-717-282-5 |
| 5 | 3741 | 97.7 | 739 | 9 | US-09-912-157-8 |
| 6 | 3741 | 97.7 | 739 | 15 | US-10-717-282-8 |
| 7 | 3731 | 97.4 | 739 | 16 | US-10-842-006-2 |
| 8 | 3731 | 97.4 | 739 | 16 | US-10-608-449-2 |
| 9 | 3729 | 97.4 | 739 | 16 | US-10-842-006-4 |
| 10 | 3725 | 97.3 | 738 | 9 | US-09-809-567-2 |
| 11 | 3725 | 97.3 | 738 | 14 | US-10-216-156-2 |

| | | | | | |
|----|--------|------|-----|----|--------------------|
| 12 | 3725 | 97.3 | 738 | 15 | US-10-616-788-2 |
| 13 | 3708 | 96.8 | 728 | 15 | US-10-104-047-3399 |
| 14 | 3703 | 96.7 | 728 | 9 | US-09-874-503-18 |
| 15 | 3703 | 96.7 | 728 | 10 | US-09-816-744-18 |
| 16 | 3703 | 96.7 | 728 | 10 | US-09-747-259-18 |
| 17 | 3703 | 96.7 | 728 | 10 | US-09-908-827-18 |
| 18 | 3703 | 96.7 | 728 | 13 | US-10-000-157-18 |
| 19 | 3703 | 96.7 | 728 | 14 | US-10-410-927-18 |
| 20 | 3703 | 96.7 | 728 | 14 | US-10-410-374-18 |
| 21 | 3703 | 96.7 | 728 | 14 | US-10-410-552-18 |
| 22 | 3703 | 96.7 | 728 | 15 | US-10-458-442-18 |
| 23 | 3703 | 96.7 | 728 | 15 | US-10-408-385-18 |
| 24 | 3657.5 | 95.5 | 738 | 10 | US-09-863-818A-10 |
| 25 | 3657.5 | 95.5 | 738 | 16 | US-10-749-144-10 |
| 26 | 3657.5 | 95.5 | 738 | 17 | US-10-924-667-10 |
| 27 | 3208 | 83.8 | 739 | 9 | US-09-912-157-12 |
| 28 | 3208 | 83.8 | 739 | 15 | US-10-717-282-12 |
| 29 | 3176 | 82.9 | 595 | 17 | US-10-477-714-16 |
| 30 | 3170 | 82.8 | 595 | 16 | US-10-608-449-4 |
| 31 | 2515.5 | 65.7 | 554 | 15 | US-10-343-348-16 |
| 32 | 1334 | 34.8 | 296 | 15 | US-10-616-788-19 |
| 33 | 312 | 8.1 | 810 | 9 | US-09-809-567-3 |
| 34 | 312 | 8.1 | 810 | 14 | US-10-216-156-3 |
| 35 | 312 | 8.1 | 810 | 15 | US-10-616-788-3 |
| 36 | 312 | 8.1 | 866 | 9 | US-09-778-971-9 |
| 37 | 312 | 8.1 | 866 | 13 | US-10-033-522-1 |
| 38 | 312 | 8.1 | 866 | 14 | US-10-207-655-107 |
| 39 | 312 | 8.1 | 866 | 16 | US-10-742-161-10 |
| 40 | 312 | 8.1 | 866 | 16 | US-10-742-372-10 |
| 41 | 312 | 8.1 | 866 | 16 | US-10-646-308-4 |
| 42 | 312 | 8.1 | 866 | 17 | US-10-318-084-1 |
| 43 | 306 | 8.0 | 864 | 16 | US-10-742-161-2 |
| 44 | 306 | 8.0 | 864 | 16 | US-10-742-372-2 |
| 45 | 232.5 | 6.1 | 207 | 10 | US-09-863-818A-19 |

ALIGNMENTS

RESULT 1

US-09-912-157-2
; Sequence 2, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912.157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-2

Query Match 100.0%; Score 3829; DB 9; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-------------------|
| Qy | 1 | ADTCGWRKAAARPRCLVANEGVGPASRNSGLYNTTFKYDNC | Sequence 2, Appli |
| Db | 36 | ADTCGWRKAAARPRCLVANEGVGPASRNSGLYNTTFKYDNC | Sequence 5, Appli |
| Qy | 61 | TISVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGR | Sequence 8, Appli |
| Db | 96 | TISVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGR | Sequence 2, Appli |
| Qy | 121 | RTGMESQPLNKKFETDYFVKVPPFPSTKNSNHYHFFRTRACD | Sequence 4, Appli |
| | | LLILOPNLACKPFWK | Sequence 2, Appli |

Db 156 RTGMESQPLNMKPEFDYFVKVVPFSPISIKNESNYHPFFRTRACDLLLLQPDNLACKPFWK 215
Qy 181 PRNLNISQHGSDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTTETSCLLQ 240
Db 216 PRNLNISQHGSDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTTETSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
Qy 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAIFL 360
Db 336 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAIFL 395
Qy 361 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db 396 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 455
Qy 421 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIAYFYDYSCEGDVPGILDLSKTYRLM 480
Db 456 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIAYFYDYSCEGDVPGILDLSKTYRLM 515
Qy 481 DNLQCLSHLSRDHGLQEPQOHTROGSRNNYFRSKGSRSLYVAICNMHQFIDEEPWF 540
Db 516 DNLQCLSHLSRDHGLQEPQOHTROGSRNNYFRSKGSRSLYVAICNMHQFIDEEPWF 575
Qy 541 KQFVPPHPPRLRYREPVLKEDFSGVLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db 576 KQFVPPHPPRLRYREPVLKEDFSGVLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 635
Qy 601 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEG 660
Db 636 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEG 695
Qy 661 LSTDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAFL 718
Db 696 LSTDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAFL 753

RESULT 2

US-10-717-282-2

; Sequence 2, Application US/10717282

; Publication No. US20040077052A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10/717,282

; CURRENT FILING DATE: 2003-11-19

; PRIOR APPLICATION NUMBER: US/09/912,157

; PRIOR FILING DATE: 2001-07-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-717-282-2

Query Match 100.0%; Score 3829; DB 15; Length 753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 718; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADTCGRMKAAARPRLCVANEGVGPASRNSGLYNIITFKYDNCCTTYLNPVGKHVIADAQNI 60
Db 36 ADTCGRMKAAARPRLCVANEGVGPASRNSGLYNIITFKYDNCCTTYLNPVGKHVIADAQNI 95
Qy 61 TISQYACHDQAVATILMSPGALGIEFLKGFVRVILEELKSEGRQCOQILKDPKQLNSSFK 120
Db 96 TISQYACHDQAVATILMSPGALGIEFLKGFVRVILEELKSEGRQCOQILKDPKQLNSSFK 155

Qy 121 RTGMESQPLNMKPEFDYFVKVVPFSPISIKNESNYHPFFRTRACDLLLLQPDNLACKPFWK 180
Db 156 RTGMESQPLNMKPEFDYFVKVVPFSPISIKNESNYHPFFRTRACDLLLLQPDNLACKPFWK 215
Qy 181 PRNLNISQHGSDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTTETSCLLQ 240
Db 216 PRNLNISQHGSDMQVSPDHAPHNFGFRFFYLHYKLKHGPPKRTCKQEQTTTETSCLLQ 275
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
Qy 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAIFL 360
Db 336 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAIFL 395
Qy 361 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db 396 QDFCGCEVALDLWEDFSLCRGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 455
Qy 421 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIAYFYDYSCEGDVPGILDLSKTYRLM 480
Db 456 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIAYFYDYSCEGDVPGILDLSKTYRLM 515
Qy 481 DNLQCLSHLSRDHGLQEPQOHTROGSRNNYFRSKGSRSLYVAICNMHQFIDEEPWF 540
Db 516 DNLQCLSHLSRDHGLQEPQOHTROGSRNNYFRSKGSRSLYVAICNMHQFIDEEPWF 575
Qy 541 KQFVPPHPPRLRYREPVLKEDFSGVLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db 576 KQFVPPHPPRLRYREPVLKEDFSGVLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 635
Qy 601 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEG 660
Db 636 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEG 695
Qy 661 LSTDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAFL 718
Db 696 LSTDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAFL 753

RESULT 3

US-09-912-157-5

; Sequence 5, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-912-157-5

Query Match 99.7%; Score 3819; DB 9; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ADTCGRMKAAARPRLCVANEGVGPASRNSGLYNIITFKYDNCCTTYLNPVGKHVIADAQNI 60
Db 36 ADTCGRMKAAARPRLCVANEGVGPASRNSGLYNIITFKYDNCCTTYLNPVGKHVIADAQNI 95
Qy 61 TISQYACHDQAVATILMSPGALGIEFLKGFVRVILEELKSEGRQCOQILKDPKQLNSSFK 120
Db 96 TISQYACHDQAVATILMSPGALGIEFLKGFVRVILEELKSEGRQCOQILKDPKQLNSSFK 155

QY 121 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 180
DB 156 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 215
QY 181 PRNLNISOHSDMQVSPDHAPHNFGFRFFYLHYKLKHEGPPFKRTCKOEQTETTSCLLQ 240
DB 216 PRNLNISOHSDMQVSPDHAPHNFGFRFFYLHYKLKHEGPPFKRTCKOEQTETTSCLLQ 275
QY 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
DB 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
QY 301 RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
DB 336 RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
QY 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVVDKKNYKHKG 420
DB 396 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVVDKKNYKHKG 455
QY 421 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 480
DB 456 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 515
QY 481 DNLQOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDBEPDWFE 540
DB 516 DNLQOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDBEPDWFE 575
QY 541 KQFVFPFPPPLRYREPVLKFDGLVLNDVCMKPGPESDFCLKVEAAVLGATGADSPQHE 600
DB 576 KQFVFPFPPPLRYREPVLKFDGLVLNDVCMKPGPESDFCLKVEAAVLGATGADSPQHE 635
QY 601 SOHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRDSGIYDSSVPSSLSPLMEG 660
DB 636 SOHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRDSGIYDSSVPSSLSPLMEG 695
QY 661 LSTQDTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLGRSYTDLHVAAPL 718
DB 696 LSTQDTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLGRSYTDLHVAAPL 753

RESULT 4

US-10-717-282-5

; Sequence 5, Application US/10717282

; Publication No. US20040077052A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/10/717,282

; CURRENT FILING DATE: 2003-11-19

; PRIOR APPLICATION NUMBER: US/09/912,157

; PRIOR FILING DATE: 2001-07-24

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 753

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-717-282-5

Query Match 99.7%; Score 3819; DB 15; Length 753;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 60

DB 36 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 95

QY 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVRIEELKSEGRQCOOLILKDPKQNLNSFK 120

DB 96 TISQYACHDQVAVTILWSPGALGIEFLKGRFVRIEELKSEGRQCOOLILKDPKQNLNSFK 155
QY 121 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 180
DB 156 RTGMSOPFLNMKFETDYFKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWK 215
QY 181 PRNLNISOHSDMQVSPDHAPHNFGFRFFYLHYKLKHEGPPFKRTCKOEQTETTSCLLQ 240
DB 216 PRNLNISOHSDMQVSPDHAPHNFGFRFFYLHYKLKHEGPPFKRTCKOEQTETTSCLLQ 275
QY 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
DB 276 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 335
QY 301 RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 360
DB 336 RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQNMVNVQCFAYFL 395
QY 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVVDKKNYKHKG 420
DB 396 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKIFVVDKKNYKHKG 455
QY 421 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 480
DB 456 RGSKGELFLVAVSAIAEKLROAKOSSAALSKEIANYFYDYSCGDPVGIILDLSTKYRLM 515
QY 481 DNLQOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDBEPDWFE 540
DB 516 DNLQOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKGSRSLYVAICNNHQFIDBEPDWFE 575
QY 541 KQFVFPFPPPLRYREPVLKFDGLVLNDVCMKPGPESDFCLKVEAAVLGATGADSPQHE 600
DB 576 KQFVFPFPPPLRYREPVLKFDGLVLNDVCMKPGPESDFCLKVEAAVLGATGADSPQHE 635
QY 601 SOHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRDSGIYDSSVPSSLSPLMEG 660
DB 636 SOHGLDQDGEARPALDGSAAALQPLHTVTKAGSPDMRDSGIYDSSVPSSLSPLMEG 695
QY 661 LSTQDTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLGRSYTDLHVAAPL 718
DB 696 LSTQDTTSSLTESVSSSSGLGEEPPALPKLLSSGCKADLGRSYTDLHVAAPL 753

RESULT 5

US-09-912-157-8

; Sequence 8, Application US/09912157

; Patent No. US20020165348A1

; GENERAL INFORMATION:

; APPLICANT: Presnell, Scott R.

; APPLICANT: Kuestner, Rolf E.

; APPLICANT: Gao, Zeren

; TITLE OF INVENTION: Human Cytokine Receptor

; FILE REFERENCE: 00-49

; CURRENT APPLICATION NUMBER: US/09/912,157

; CURRENT FILING DATE: 2001-07-23

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 739

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-157-8

Query Match 97.7%; Score 3741; DB 9; Length 739;

Best Local Similarity 98.1%; Pred. No. 0;

Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

QY 1 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 60

DB 36 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNTFFKYDNCCTTYLNPVGVKHVIADAQNI 81

QY 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVRIEELKSEGRQCOOLILKDPKQNLNSFK 120

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Db      82  TISQYACHDOVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCQQLILKDPKQLNSSFK 141
Qy      121  RTGMSOPFLNMKFETDYFVKVVPFPPSIKNESNYHPFFFRTRACDILLQDPNLACKPFWK 180
Db      142  RTGMSOPFLNMKFETDYFVKVVPFPPSIKNESNYHPFFFRTRACDILLQDPNLACKPFWK 201
Qy      181  PRNLNISOHGSQDMQVSDFHAPHNFGPRFFYLHYLKHGEPFKRKTCKQEQTTTSCLLQ 240
Db      202  PRNLNISOHGSQDMQVSDFHAPHNFGPRFFYLHYLKHGEPFKRKTCKQEQTTTSCLLQ 261
Qy      241  NVSPGDYIIELVDNTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db      262  NVSPGDYIIELVDNTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy      301  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 360
Db      322  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 381
Qy      361  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db      382  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 441
Qy      421  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 480
Db      442  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 501
Qy      481  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 540
Db      502  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 561
Qy      541  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db      562  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy      601  SQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 660
Db      622  SQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 681
Qy      661  LSTDQTETSSLTESVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 718
Db      682  LSTDQTETSSLTESVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 739
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RESULT 6

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US-10-717-282-8
; Sequence 8, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-717-282-8
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Query Match          97.7%; Score 3741; DB 15; Length 739;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 704; Conservative 0; Mismatches 0; Indels 14; Gaps 1;

Qy      1  ADTCGWRMKAARPRCLVCVANEVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 60
Db      36  ADTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 81
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Qy      61  TISQYACHDOVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCQQLILKDPKQLNSSFK 120
Db      82  TISQYACHDOVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCQQLILKDPKQLNSSFK 141
Qy      121  RTGMSOPFLNMKFETDYFVKVVPFPPSIKNESNYHPFFFRTRACDILLQDPNLACKPFWK 180
Db      142  RTGMSOPFLNMKFETDYFVKVVPFPPSIKNESNYHPFFFRTRACDILLQDPNLACKPFWK 201
Qy      181  PRNLNISOHGSQDMQVSDFHAPHNFGPRFFYLHYLKHGEPFKRKTCKQEQTTTSCLLQ 240
Db      202  PRNLNISOHGSQDMQVSDFHAPHNFGPRFFYLHYLKHGEPFKRKTCKQEQTTTSCLLQ 261
Qy      241  NVSPGDYIIELVDNTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db      262  NVSPGDYIIELVDNTNTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy      301  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 360
Db      322  RKQOENIYSHLDESESSSTYTAALPRERLRPRPKVFLCYSSKDGQGNHNVVQCFAFL 381
Qy      361  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 420
Db      382  QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGGG 441
Qy      421  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 480
Db      442  RSGKGELFLVAVSAIAEKLRAQAKQSSSAALSKEFIAVYFDYSCGDVPGILDSTKYRLM 501
Qy      481  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 540
Db      502  DNLPLCSHLHSRDHGLQEPGQHTROGSRNNYFRSKSGRSLYVAICNMHOFIDEEPWF 561
Qy      541  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db      562  KQFVPPHPPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy      601  SQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 660
Db      622  SQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVSPSELSPLMEG 681
Qy      661  LSTDQTETSSLTESVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 718
Db      682  LSTDQTETSSLTESVSSSGLGEEPPALPKLLSSGSKADLCGRSYTDELHVAAPL 739
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RESULT 7

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US-10-842-006-2
; Sequence 2, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MEI03-071PRM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-2
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Query Match          97.4%; Score 3731; DB 16; Length 739;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 702; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy      1  ADTCGWRMKAARPRCLVCVANEVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 60
Db      36  ADTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGHVIAQAQNI 81
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Qy 61 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSSFK 120
Db 82 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSSFK 141
Qy 121 RTGMESQPFLLNMKFETDYFKVVPFPPSIKNESNTHPFFFRTRACDILLQPDNLACKPFWK 180
Db 142 RTGMESQPFLLNMKFETDYFKVVPFPPSIKNESNTHPFFFRTRACDILLQPDNLACKPFWK 201
Qy 181 PRNLINISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBTETTSCILQ 240
Db 202 PRNLINISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBTETTSCILQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 262 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCAYFL 360
Db 322 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCAYFL 381
Qy 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
Db 382 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 441
Qy 421 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 480
Db 442 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 501
Qy 481 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEDPWF 540
Db 502 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEDPWF 561
Qy 541 KQFVFPHPPLRYREPVLKEDTSGLVLDVNDVCMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db 562 KQFVFPHPPLRYREPVLKEDTSGLVLDVNDVCMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy 601 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMRDSGIYDSSVPSSSELSPLMEG 660
Db 622 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMRDSGIYDSSVPSSSELSPLMEG 681
Qy 661 LSTQDTSTTSITSVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVA 718
Db 682 LSTQDTSTTSITSVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVA 739

RESULT 8
US-10-608-449-2
; Sequence 2, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: I2003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-608-449-2

Query Match 97.4%; Score 3731; DB 16; Length 739;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 702; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 1 ADTCGWRKMAAARPLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIAQAQNI 60
Db 36 ADTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIAQAQNI 81
Qy 61 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSSFK 120

Db 82 TISQACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCOQLILKDPKOLNSSFK 141
Qy 121 RTGMESQPFLLNMKFETDYFKVVPFPPSIKNESNTHPFFFRTRACDILLQPDNLACKPFWK 180
Db 142 RTGMESQPFLLNMKFETDYFKVVPFPPSIKNESNTHPFFFRTRACDILLQPDNLACKPFWK 201
Qy 181 PRNLINISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBTETTSCILQ 240
Db 202 PRNLINISQSGDMQVSDHAPHNFGFRFFYLHYKLKHEGPPKRTCKOBTETTSCILQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db 262 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCAYFL 360
Db 322 RKQOENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNMNVVQCAYFL 381
Qy 361 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 420
Db 382 QDFCGCEVALDLWEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKG 441
Qy 421 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 480
Db 442 RSGKGELFLVAVSAIAEKLROAKQSSAALSKEFIIVVCSKGMKYFVDKKNYKHKG 501
Qy 481 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEDPWF 540
Db 502 DNLQCLSHLSRDHGLQEPQOHTROGSRNRYFRSKSGRSIYVAICNMHQFIDEEDPWF 561
Qy 541 KQFVFPHPPLRYREPVLKEDTSGLVLDVNDVCMCKPGPESDFCLKVEAAVLGATGADSOHE 600
Db 562 KQFVFPHPPLRYREPVLKEDTSGLVLDVNDVCMCKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy 601 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMRDSGIYDSSVPSSSELSPLMEG 660
Db 622 SOHGLDQDGEARPALDGSAAALQPLLHTVTKAGSPDMRDSGIYDSSVPSSSELSPLMEG 681
Qy 661 LSTQDTSTTSITSVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVA 718
Db 682 LSTQDTSTTSITSVSSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVA 739

RESULT 9
US-10-842-006-4
; Sequence 4, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruyi-Bing
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: MF103-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-4

Query Match 97.4%; Score 3729; DB 16; Length 739;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 701; Conservative 1; Mismatches 1; Indels 14; Gaps 1;
Qy 2 DTCCWRKMAAARPLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIAQAQNI 61
Db 37 DTCCWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIAQAQNI 82

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Qy 62 ISOYACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKOPKQLNSFFKR 121
Db 83 ISOYACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKOPKQLNSFFKR 142
Qy 122 TGMESQPFLLNMKFETDYFVKVVPFPPSIKNESNYHPFFRTRACDILLQPNLACKPFWKP 181
Db 143 TGMESQPFLLNMKFETDYFVKVVPFPPSIKNESNYHPFFRTRACDILLQPNLACKPFWKP 202
Qy 182 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHGPPKRTCKOEQTETTSCLLON 241
Db 203 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHGPPKRTCKOEQTETTSCLLON 262
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAFATLFTVMCR 301
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAFATLFTVMCR 322
Qy 302 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
Db 323 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
Qy 362 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGELFLVAVSAIAEKLROAKOSSAALSKEFTAVYFDYSCGDVPGIILDLSTKYRLMD 481
Db 443 GSGKGELFLVAVSAIAEKLROAKOSSAALSKEFTAVYFDYSCGDVPGIILDLSTKYRLMD 502
Qy 482 NLPQLCSHLHRDGLQBPQOHTRQGSRRNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 541
Db 503 NLPQLCSHLHRDGLQBPQOHTRQGSRRNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 562
Qy 542 QFVFPHPPLRYRREPVLKFDPSGLVLDVNMCKPGPESDFCLKVEAAVLGATGPADSQSHES 601
Db 563 QFVFPHPPLRYRREPVLKFDPSGLVLDVNMCKPGPESDFCLKVEAPVLGATGPADSQSHES 622
Qy 602 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 661
Db 623 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 682
Qy 662 STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTYDELHVAAPL 718
Db 683 STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTYDELHVAAPL 739

RESULT 10
US-09-567-2
; Sequence 2, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; CURRENT FILING DATE: 2001-03-15
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-567-2

Query Match 97.3%; Score 3725; DB 9; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTCGWRKKAARPRLCVANEGVGPASRNSGLNYITFKYDNCCTTYLNPVKGHVIAQAQNIIT 61
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Db 37 DTCGWR-----GVGPASRNSGLNYITFKYDNCCTTYLNPVKGHVIAQAQNIIT 82
Qy 62 ISOYACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKOPKQLNSFFKR 121
Db 83 ISOYACHDOVAVTILWSPGALGIEFLKGRFVILBELKSEGRQCOQLILKOPKQLNSFFKR 142
Qy 122 TGMESQPFLLNMKFETDYFVKVVPFPPSIKNESNYHPFFRTRACDILLQPNLACKPFWKP 181
Db 143 TGMESQPFLLNMKFETDYFVKVVPFPPSIKNESNYHPFFRTRACDILLQPNLACKPFWKP 202
Qy 182 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHGPPKRTCKOEQTETTSCLLON 241
Db 203 RNLNISQHGSDMOVSFDHAPHNFGFRFFYLHYKLKHGPPKRTCKOEQTETTSCLLON 262
Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAFATLFTVMCR 301
Db 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVISAFATLFTVMCR 322
Qy 302 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
Db 323 KQOENIYSHLDESSSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
Qy 362 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 421
Db 383 DFCCEVALDLWEDFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKHGGGR 442
Qy 422 GSGKGELFLVAVSAIAEKLROAKOSSAALSKEFTAVYFDYSCGDVPGIILDLSTKYRLMD 481
Db 443 GSGKGELFLVAVSAIAEKLROAKOSSAALSKEFTAVYFDYSCGDVPGIILDLSTKYRLMD 502
Qy 482 NLPQLCSHLHRDGLQBPQOHTRQGSRRNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 541
Db 503 NLPQLCSHLHRDGLQBPQOHTRQGSRRNYFRSKGSRSLYVAICNNHQFIDEEPWFKEK 562
Qy 542 QFVFPHPPLRYRREPVLKFDPSGLVLDVNMCKPGPESDFCLKVEAAVLGATGPADSQSHES 601
Db 563 QFVFPHPPLRYRREPVLKFDPSGLVLDVNMCKPGPESDFCLKVEAPVLGATGPADSQSHES 622
Qy 602 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 661
Db 623 QHGGLDODGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSLSLPLMEGL 682
Qy 662 STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTYDELHVAAP 717
Db 683 STDQTETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTYDELHVAAP 738

RESULT 11
US-10-216-156-2
; Sequence 2, Application US/10216156
; Publication No. US20030099980A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; CURRENT FILING DATE: 2002-08-08
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-156-2

Query Match 97.3%; Score 3725; DB 14; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
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Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTCGRMKAAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGRHVIADAQNIT 61
Db |||||
Qy 37 DTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGRHVIADAQNIT 82
Db |||||

Qy 62 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 121
Db |||||

Qy 83 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 142
Db |||||

Qy 122 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWKP 181
Db |||||

Qy 143 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWKP 202
Db |||||

Qy 182 RNLNISQHGSDMQVSDPHAPNFGFRFYLYHKHEGPPFKRKTCKOBTETTSCLLQN 241
Db |||||

Qy 203 RNLNISQHGSDMQVSDPHAPNFGFRFYLYHKHEGPPFKRKTCKOBTETTSCLLQN 262
Db |||||

Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 301
Db |||||

Qy 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 322
Db |||||

Qy 302 KQOENIYSHLDESSSSTVTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
Db |||||

Qy 323 KQOENIYSHLDESSSSTVTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
Db |||||

Qy 362 DFCCEVALDWEDEFSLCREGQREWVIOKHESQFIIVVCSKGMKYFVDKKNYKHKGGR 421
Db |||||

Qy 383 DFCCEVALDWEDEFSLCREGQREWVIOKHESQFIIVVCSKGMKYFVDKKNYKHKGGR 442
Db |||||

Qy 422 GSGGELFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGQVPGILDSTKYRLMD 481
Db |||||

Qy 443 GSGGELFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGQVPGILDSTKYRLMD 502
Db |||||

Qy 482 NLPQLCSHLHSDHGLQEPGQHTQGSRRNYFRSKSGRSLYVAICNMHQFIDEEDPWFKEK 541
Db |||||

Qy 503 NLPQLCSHLHSDHGLQEPGQHTQGSRRNYFRSKSGRSLYVAICNMHQFIDEEDPWFKEK 562
Db |||||

Qy 542 QFVFPHPPLRYRREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 601
Db |||||

Qy 563 QFVFPHPPLRYRREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 622
Db |||||

Qy 602 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGLYDSSVPSSSELSLPLMBGL 661
Db |||||

Qy 623 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGLYDSSVPSSSELSLPLMBGL 682
Db |||||

Qy 662 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTSYTDELHAVAP 717
Db |||||

Qy 683 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTSYTDELHAVAP 738
Db |||||

RESULT 12

US-10-616-788-2
; Sequence 2, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/39525
; CURRENT APPLICATION NUMBER: US/10/616,788
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-616-788-2

Query Match 97.3%; Score 3725; DB 15; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 700; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 2 DTCGRMKAAARPRLCVANEGVGPASRNSGLYNTFKYDNCCTTYLNPVGRHVIADAQNIT 61
Db |||||

Qy 37 DTCGWR-----GVGPASRNSGLYNTFKYDNCCTTYLNPVGRHVIADAQNIT 82
Db |||||

Qy 62 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 121
Db |||||

Qy 83 ISOYACHDQAVATILWSPGALGIEFLKGRFVILEELKSEGRQCQOLILKDPKQLNSSFKR 142
Db |||||

Qy 122 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWKP 181
Db |||||

Qy 143 TGMESQPLNMKFTDYFVKVVPFPPSIKNESNYHPPFFRTRACDILLQPDNLACKPFWKP 202
Db |||||

Qy 182 RNLNISQHGSDMQVSDPHAPNFGFRFYLYHKHEGPPFKRKTCKOBTETTSCLLQN 241
Db |||||

Qy 203 RNLNISQHGSDMQVSDPHAPNFGFRFYLYHKHEGPPFKRKTCKOBTETTSCLLQN 262
Db |||||

Qy 242 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 301
Db |||||

Qy 263 VSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAFATLFTVMCR 322
Db |||||

Qy 302 KQOENIYSHLDESSSSTVTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 361
Db |||||

Qy 323 KQOENIYSHLDESSSSTVTAALPRERLRPRPKVFLCYSSKDGQNHMNVVQCFAYFLQ 382
Db |||||

Qy 362 DFCCEVALDWEDEFSLCREGQREWVIOKHESQFIIVVCSKGMKYFVDKKNYKHKGGR 421
Db |||||

Qy 383 DFCCEVALDWEDEFSLCREGQREWVIOKHESQFIIVVCSKGMKYFVDKKNYKHKGGR 442
Db |||||

Qy 422 GSGGELFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGQVPGILDSTKYRLMD 481
Db |||||

Qy 443 GSGGELFLVAVSAIAEKLROAKOSSAALSKEFTAVFYDSCGQVPGILDSTKYRLMD 502
Db |||||

Qy 482 NLPQLCSHLHSDHGLQEPGQHTQGSRRNYFRSKSGRSLYVAICNMHQFIDEEDPWFKEK 541
Db |||||

Qy 503 NLPQLCSHLHSDHGLQEPGQHTQGSRRNYFRSKSGRSLYVAICNMHQFIDEEDPWFKEK 562
Db |||||

Qy 542 QFVFPHPPLRYRREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 601
Db |||||

Qy 563 QFVFPHPPLRYRREPVLKFDPSGLVNDVMCKPGPESDFCLKVEAPVLGATGPADSOHES 622
Db |||||

Qy 602 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGLYDSSVPSSSELSLPLMBGL 661
Db |||||

Qy 623 QHGGLDQGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGLYDSSVPSSSELSLPLMBGL 682
Db |||||

Qy 662 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTSYTDELHAVAP 717
Db |||||

Qy 683 STDQETSSLTESVSSSSGLGEEPPALPSKLLSSGCKADLGCRTSYTDELHAVAP 738
Db |||||

RESULT 13

US-10-104-047-3399
; Sequence 3399, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3399
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-104-047-3399

Query Match 96.8%; Score 3708; DB 15; Length 728;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 21 EGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAGNITISQYACHDQVAVTILMSPG 80
Db :|||||
Qy 31 QGVGPASRNSGLYNTFKYDNCCTTYLNPVGKHVIADAGNITISQYACHDQVAVTILMSPG 90
Db :|||||
Qy 81 ALGIEFLKGRFVRIIEELKSEGRQCOQLILKDPKQLNSPFRKTGMESQFFLNMKFETDYFV 140
Db :|||||
Qy 91 ALGIEFLKGRFVRIIEELKSEGRQCOQLILKDPKQLNSPFRKTGMESQFFLNMKFETDYFV 150
Db :|||||
Qy 141 KVPFPPIKESNTHPFRFRTRACDILLIOPNLACKPFWKPRNLIISQHGSDMQVSDHA 200
Db :|||||
Qy 151 KVPFPPIKESNTHPFRFRTRACDILLIOPNLACKPFWKPRNLIISQHGSDMQVSDHA 210
Db :|||||
Qy 201 PHNFGFRFFYLHYKLKHEGPFKRTCKOEQTETTSCLLQNVSPGDYIIELVDDTNTTRK 260
Db :|||||
Qy 211 PHNFGFRFFYLHYKLKHEGPFKRTCKOEQTETTSCLLQNVSPGDYIIELVDDTNTTRK 270
Db :|||||
Qy 261 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSS 320
Db :|||||
Qy 271 VMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDESSSS 330
Db :|||||
Qy 321 TYTAALPRERLRPRPKVFLCYSSKQGNHNVQCFAYFLQDFCGCEVALDLWEDFSLCR 380
Db :|||||
Qy 331 TYTAALPRERLRPRPKVFLCYSSKQGNHNVQCFAYFLQDFCGCEVALDLWEDFSLCR 390
Db :|||||
Qy 381 EGQREWIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKL 440
Db :|||||
Qy 391 EGQREWIQKHESQFIIVVCSKGMKYFVDKKNYKHKGGRSGKGLFLVAVSAIAEKL 450
Db :|||||
Qy 441 RQAKQSSAALSKEFIAYFYDYSCEGVPGLLDLSTKYRLMDNLPLQCSHLHSRDHGLQEP 500
Db :|||||
Qy 451 RQAKQSSAALSKEFIAYFYDYSCEGVPGLLDLSTKYRLMDNLPLQCSHLHSRDHGLQEP 510
Db :|||||
Qy 501 GQHTQSSRRNYFRSKGRSLYVAICNMHQFIDEEDPWFEKQFVFPFPPPLRYREPVLK 560
Db :|||||
Qy 511 GQHTQSSRRNYFRSKGRSLYVAICNMHQFIDEEDPWFEKQFVFPFPPPLRYREPVLK 570
Db :|||||
Qy 561 FDSGLVLNDVCKPGPSDFCLKVEAAVLGATGADSOHESQHGGLQDGEARPALDQSA 620
Db :|||||
Qy 571 FDSGLVLNDVCKPGPSDFCLKVEAAVLGATGADSOHESQHGGLQDGEARPALDQSA 630
Db :|||||
Qy 621 ALQPLHTVKAGSPDMPRDSGIYDSSVPSSSELSLPLMEGLSTDTQETSSLITESVSSSG 680
Db :|||||
Qy 631 ALQPLHTVKAGSPDMPRDSGIYDSSVPSSSELSLPLMEGLSTDTQETSSLITESVSSSG 690
Db :|||||
Qy 681 LGEDEPPALPSKLLSSGSKADLGRSVTDBLHVAVPL 718
Db :|||||
Qy 691 LGEDEPPALPSKLLSSGSKADLGRSVTDBLHVAVPL 728
Db :|||||

RESULT 14

US-09-874-503-18
Sequence 18, Application US/09874503
Patent No. US20020177188A1

GENERAL INFORMATION:

APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hymowitz, Sarah G.
APPLICANT: Tumas, Daniel
APPLICANT: Starovasnik, Melissa A.
APPLICANT: VanLookeren, Menno

APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P3 (US)
CURRENT APPLICATION NUMBER: US/09/874, 503
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/253, 646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/244, 072
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 60/242, 837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/175, 481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 60/191, 007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/213, 807
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 60/172, 096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/138, 387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: US 60/134, 287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/131, 022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: US 60/130, 232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/113, 621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/085, 579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 09/854, 208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854, 280
PRIOR FILING DATE: 2001-05-20
PRIOR APPLICATION NUMBER: US 09/816, 744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/747, 259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/644, 848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/380, 142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/380, 138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 09/311, 832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US PCT/US99/31274
PRIOR FILING DATE: 1999-12-30

; PRIOR APPLICATION NUMBER: US PCT/US99/10733
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: US PCT/US99/05028
 ; PRIOR FILING DATE: 1999-03-08
 ; NUMBER OF SEQ ID NOS: 39
 ; SEQ ID NO 18
 ; LENGTH: 728
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-874-503-18

Query Match 96.7%; Score 3703; DB 9; Length 728;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

 Qy 7 RMKAAAPRLCVANE-GVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 65
 Db 3 RASAGVPAIFVSGEQGVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 62

 Qy 66 ACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCQOLILKDPKQLNSSFKRTGME 125
 Db 63 ACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCQOLILKDPKQLNSSFKRTGME 122

 Qy 126 SOPFLNMKFETDYFVKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 185
 Db 123 SOPFLNMKFETDYFVKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 182

 Qy 186 ISQ-----HGSDMQVDFDHAPHNFGFRFFYLHYKLHKGEPFKRTCKQEQTT 232
 Db 183 ISQHGSDMQVDFDHAPHNFGFRFFYLHYKLHKGEPFKRTCKQEQTT 242

 Qy 233 ETTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
 Db 243 EMTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

 Qy 293 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 352
 Db 303 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 362

 Qy 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKK 412
 Db 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKK 422

 Qy 413 NYKHGGGRGSGKGLFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 472
 Db 423 NYKHGGGRGSGKGLFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 482

 Qy 473 LSTKYRLMDNLPOLCASHLHSDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFI 532
 Db 483 LSTKYRLMDNLPOLCASHLHSDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFI 542

 Qy 533 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVWCKPSPDPRDSGIYDSSVPSSE 592
 Db 543 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVWCKPSPDPRDSGIYDSSVPSSE 602

 Qy 593 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLLHTVKGAGSPDPRDSGIYDSSVPSSE 652
 Db 603 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLLHTVKGAGSPDPRDSGIYDSSVPSSE 662

 Qy 653 LSLPLMEGLSTDQTTSTSTESVSSSGLGEPEPALPSKLLSSGCKADLGCRTYTDL 712
 Db 663 LSLPLMEGLSTDQTTSTSTESVSSSGLGEPEPALPSKLLSSGCKADLGCRTYTDL 722

 Qy 713 HAVAPL 718
 Db 723 HAVAPL 728

RESULT 15
 US-09-816-744-18
 ; Sequence 18, Application US/09816744
 ; Publication No. US20030003546A1
 ; GENERAL INFORMATION:

; APPLICANT: Chen, Jian
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Li, Hanzhong
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: VanLookeren, Menno
 ; APPLICANT: Vandlen, Richard
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William
 ; APPLICANT: Yansura, Daniel
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
 ; FILE REFERENCE: P1381R1C1P2(US)
 ; CURRENT APPLICATION NUMBER: US/09/816,744
 ; CURRENT FILING DATE: 2001-03-22
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 39
 ; SEQ ID NO 18
 ; LENGTH: 728
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-816-744-18

Query Match 96.7%; Score 3703; DB 10; Length 728;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 702; Conservative 2; Mismatches 8; Indels 14; Gaps 2;

 Qy 7 RMKAAAPRLCVANE-GVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 65
 Db 3 RASAGVPAIFVSGEQGVGPASRNSGLYNTIFKVDNCTTYLNPVKGKVIADAQNITISQY 62

 Qy 66 ACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCQOLILKDPKQLNSSFKRTGME 125
 Db 63 ACHDOVAVTILWSPGALGIEFLKGRVILEELKSEGRQCQOLILKDPKQLNSSFKRTGME 122

 Qy 126 SOPFLNMKFETDYFVKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 185
 Db 123 SOPFLNMKFETDYFVKVVPFPIKESNYHFFRTRACDILLQPDNLACKPFWKPRNLN 182

 Qy 186 ISQ-----HGSDMQVDFDHAPHNFGFRFFYLHYKLHKGEPFKRTCKQEQTT 232
 Db 183 ISQHGSDMQVDFDHAPHNFGFRFFYLHYKLHKGEPFKRTCKQEQTT 242

 Qy 233 ETTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 292
 Db 243 EMTSCLLQNVSPGDIYIELVDVDTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAF 302

 Qy 293 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 352
 Db 303 ATLFTVMCRKQKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHNV 362

 Qy 353 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKK 412
 Db 363 VQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKK 422

 Qy 413 NYKHGGGRGSGKGLFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 472
 Db 423 NYKHGGGRGSGKGLFLVAVSAEKLRAQKSSAALSKEFIAYFYDYSCEGDVPGILD 482

 Qy 473 LSTKYRLMDNLPOLCASHLHSDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFI 532
 Db 483 LSTKYRLMDNLPOLCASHLHSDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFI 542

 Qy 533 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVWCKPSPDPRDSGIYDSSVPSSE 592
 Db 543 DEEDPWFEKQVFPFHPPLRYREPVLKFDGLVNDVWCKPSPDPRDSGIYDSSVPSSE 602

 Qy 593 GPADSQHSQHGGLDQDGEARPALDGSAAALQPLLHTVKGAGSPDPRDSGIYDSSVPSSE 652

| | | | |
|----|-----|---|-----|
| Db | 603 | GPADSQHESQHGGLDQDGEARPALDGSAAALQPLLHTVKAGSPDMPRDSGIYDSSVPSSSE | 662 |
| Qy | 653 | LSLPLMEGLSTDQETSTSLTESVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDEL | 712 |
| Db | 663 | LSLPLMEGLSTDQETSTSLTESVSSSGLGEEPPALPSKLLSSGCKADLGCRSYTDEL | 722 |
| Qy | 713 | HAVAPL | 718 |
| Db | 723 | HAVAPL | 728 |

Search completed: August 9, 2005, 11:54:41
Job time : 106.966 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2005, 11:37:17 ; Search time 28.7981 Seconds
(without alignments)
2398.896 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753
Perfect score: 3829
Sequence: 1 ADTCGRWKAARPLCVAN.....CKADLGCRSYDELHVAAPL 718

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------|--------------------|
| 1 | 3005 | 78.5 | 564 | T42695 | hypothetical prote |
| 2 | 170.5 | 4.5 | 846 | T27282 | hypothetical prote |
| 3 | 126.5 | 3.3 | 718 | T30113 | hypothetical prote |
| 4 | 117 | 3.1 | 757 | T09081 | telomere-associate |
| 5 | 116.5 | 3.0 | 901 | T83781 | transposase (08) / |
| 6 | 110 | 2.9 | 535 | T17212 | hypothetical prote |
| 7 | 110 | 2.9 | 592 | T49239 | vesicle transport |
| 8 | 110 | 2.9 | 917 | T04661 | hypothetical prote |
| 9 | 109 | 2.8 | 998 | T37627 | protein-tyrosine k |
| 10 | 107.5 | 2.8 | 938 | T49071 | protein kinase - m |
| 11 | 107.5 | 2.8 | 3788 | T13960 | beige protein homo |
| 12 | 107.5 | 2.8 | 3942 | T42730 | Basoon protein - |
| 13 | 106.5 | 2.8 | 638 | T86477 | protein F1504.27 [|
| 14 | 106 | 2.8 | 3788 | T30851 | lysosomal traffick |
| 15 | 105 | 2.7 | 901 | TJ6093 | dead ringer nuclea |
| 16 | 105 | 2.7 | 1571 | T14155 | zinc finger protei |
| 17 | 104 | 2.7 | 1462 | T36182 | protein-tyrosine-p |
| 18 | 103.5 | 2.7 | 663 | T43987 | GTPase-activating |
| 19 | 103.5 | 2.7 | 930 | T84668 | Argonaute (AGO1)-1 |
| 20 | 102 | 2.7 | 813 | T84748 | ABR protein 2 - hu |
| 21 | 102 | 2.7 | 859 | T49307 | 98K GTPase-activat |
| 22 | 102 | 2.7 | 1448 | T412007 | Subtilase family p |
| 23 | 101.5 | 2.7 | 822 | T47485 | ABR protein 1 - hu |
| 24 | 101.5 | 2.7 | 1639 | T50119 | probable sensory t |
| 25 | 101 | 2.6 | 641 | T05497 | hypothetical prote |
| 26 | 101 | 2.6 | 664 | T51247 | ARR2 protein limpo |
| 27 | 101 | 2.6 | 1275 | T43985 | nucleotide exchang |
| 28 | 100.5 | 2.6 | 1007 | T24643 | hypothetical prote |
| 29 | 99.5 | 2.6 | 657 | T96949 | serine/threonine p |

ALIGNMENTS

RESULT 1

T42695
hypothetical protein DKFp434N1928.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T42695
R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z22230
A:Accession: T42695
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-564 <AAA>
A:Cross-references: UNIPROT:Q9UFA0; EMBL:AL133097
A:Experimental source: adult testis; clone DKFp434N1928
C:Genetics:
A:Note: DKFp434N1928.1

Query Match 78.5%; Score 3005; DB 2; Length 564;
Best Local Similarity 99.8%; Pred. No. 2.7e-232; Indels 0; Gaps 0;
Matches 563; Conservative 0; Mismatches 1;

| | | | |
|----|-----|---|-----|
| Qy | 155 | HPFFRTRACDLLLQPDNLACKPFWKPRNLNLSQHGSDMQVSDHAPNFGFRFFYLHYK | 214 |
| Db | 1 | HPFFRTRACDLLLQPDNLACKPFWKPRNLNLSQHGSDMQVSDHAPNFGFRFFYLHYK | 60 |
| Qy | 215 | LKHEGPFKRKCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA | 274 |
| Db | 61 | LKHEGPFKRKCKQEQTTETTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA | 120 |
| Qy | 275 | GPIRAVAITVPLVWISAFATLFTWCRKKQENIYSHLDEESSESTTTAALPRRLRPR | 334 |
| Db | 121 | GPIRAVAITVPLVWISAFATLFTWCRKKQENIYSHLDEESSESTTTAALPRRLRPR | 180 |
| Qy | 335 | PKVFLCYSSKDGQNHMNVVQCFAVFLQDFCCEVALDLWEDFSLCREGQREWVIQKHES | 394 |
| Db | 181 | PKVFLCYSSKDGQNHMNVVQCFAVFLQDFCCEVALDLWEDFSLCREGQREWVIQKHES | 240 |
| Qy | 395 | QFIIIVCSKGMKYFVDKQYKHKGGRSGKGEFLVAVSAIAEKLRAQKQSSAALSXF | 454 |
| Db | 241 | QFIIIVCSKGMKYFVDKQYKHKGGRSGKGEFLVAVSAIAEKLRAQKQSSAALSXF | 300 |
| Qy | 455 | IATVFDYSCGEGVPGILDLSTKYRLMDNLPCSLHLHRDGLQPGQHTROGSRNRYPR | 514 |
| Db | 301 | IATVFDYSCGEGVPGILDLSTKYRLMDNLPCSLHLHRDGLQPGQHTROGSRNRYPR | 360 |
| Qy | 515 | SKSGRLVVAICNMHQFIDEEPDMFEKQFVFPHPPLAYREPVLEKFSGLVNDVMCKP | 574 |
| Db | 361 | SKSGRLVVAICNMHQFIDEEPDMFEKQFVFPHPPLAYREPVLEKFSGLVNDVMCKP | 420 |
| Qy | 575 | GPESDFCLKVEAAVLGATGPADSQHSQHGLDQDGEPALDGSAAALQPLLHTVAGSP | 634 |

A;Reference number: Z16557; MUID:98198830; PMID:9539423
A;Accession: T09081
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-757 <SAN>
A;Cross-references: UNIPROT:O13399; EMBL:AF030885; NID:g2642221; PID:g2642222
A;Experimental source: strain FB2
C;Genetics:
A;Gene: UTASrecQ
C;Keywords: DNA binding

Query Match 3.1%; Score 117; DB 2; Length 757;
Best Local Similarity 20.4%; Pred. No. 0.6;
Matches 111; Conservative

Qy 233 ETTSCLLQNVSPGDIYIELVDVDTYTRKVMHYALKVHSPWAGPIRAV---AIVPL-- 286
Db 77 ETTILILPTVALRANMLAKLDVNM-----IRYHVQP-GSKKAAPILVSTAAITLAPKE 131
Qy 287 -----VVISAFATLFTVMCKKQENIYSHLDEESSESTYTAALP----- 327
Db 132 YANRLQOORLDRIVIDECHLTITARSYRSMQQLAWHVRDVTQVWLATLPIFEDA 191
Qy 328 --RERLRPRKVP-----LCYSSKDGQNHMNVQCF-AYFLQDFCGCEVALDWMEDF 376
Db 192 FISHNKLTKPLIVRESTNRSLCYSVRTAEHRMSGMTCYDAVRVVD--ECHARTDIW--- 246
Qy 377 SLCREGQREWIQIHESQFIIVVCSGKMKYFVDK-----KNYKHGGGSGS----- 423
Db 247 ----NGQD-----RIIVYCTS--KELVARLAEMLCGAAYSESSEADKAAIIQ 290
Qy 424 ----GKELPLVAVSAIAEKLQAKQSSAALSXFIAYFYSCGQVPGIL--DLSTKY 477
Db 291 DWICGKSPVIVATSA-----LGVFPYPHVRFVHLLGPDLLTDF 331
Qy 478 -----RLMDNLPOLCSHLHSDHGLQFPQGHOTRQGRNRNFRS 515
Db 332 SQESGRAGDGPAPESILLAGPQLDDRAP-ASGRASSAEKGVAPG---ADKEAMQLYRS 387
Qy 516 KSGRSLYVAICNMQOFDEEDPWEKQFVPHPPPLRPREVLEKFDGLVINDVMCKPG 575
Db 388 RK-----YCLRGVLSQLQDRSDW-----RWCMEGDQLCSVC 419
Qy 576 PESDFCLKVEAVLGCATGPADSOH---ESQHGGLDQDGEARPALDGSAAOLPLHTVKAG 632
Db 420 PGHHF-----QARGGQDQFHTAPAQAGDPSQGRHPSMHGSS--HPSMH----- 463
Qy 633 SPSPMDPRDSGIYDSSVPSSE-LSLPLMEGLSTDTQTSTSLTESVSSS---SGLGEEPEPPA 688
Db 464 -----GSSHPSSHSGSHPSINGSHPSIHGSS-HPSIHGSGQHGQRRKQKQPD 510
Qy 689 LPSK 692
Db 511 PPSE 514

RESULT 5
F83781
transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus ha
A;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F83781
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83781
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-901 <STO>
A;Cross-references: UNIPROT:Q9BE04; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA8047
A;Experimental source: strain C-125
C;Genetics:

A;Gene: BH1054

Query Match 3.0%; Score 116.5; DB 2; Length 901;
Best Local Similarity 19.6%; Pred. No. 0.85;
Matches 112; Conservative

Qy 26 ASRNSGLYNTFKYDNCCTTVLNPVGHVIAIDAQNIITISQY-ACHDQVAVTILWSPGALGI 84
Db 333 ALKESGL-----PLPKTLIADAGVGSSESNVYAMADELFETLIPS----- 371
Qy 85 EFLKPRVILEELKSEGR-----OCQOL--ILKDPKQLNSFKRTGMESQPLNNKF 134
Db 372 ---HTFR--OEQRKSPAKKFPHPYNWRCDETDVYWCNQRKVSFKYTKRTDY---GY 423
Qy 135 ETDYFV-----KVVPF-PSI-----KNESNYHPFFRTRACDILLQPDNLACPFKWKPR 182
Db 424 ARDFKVVCESECGCPFPKCTKARGNRQVHNPVY-----EELKAKHQKLIK 471
Qy 183 NLNISOHG-----SDMQVSPDHAPHNFGFRFFLYHKLHKGEPKPKCKCKQEQTTET 234
Db 472 ---SEGRITLYQKRTDVSFVGHVQNLGFRHLRGK----- 507
Qy 235 TSCLLQNVSPGDIYIELVDVDTNTRKVMHYALKVHSPWAGPIRAVAITVPLVVIS-AFA 293
Db 508 -----ESVIELGLVALAHNL 524
Qy 294 TLFTVMCRKQENIYSHLDEESSESTYTAALPRERLRPRPKVFLCYSSKDGQNHMNV 353
Db 525 KRATVDRSRKPKTNQHNREN-----RIKRF-----SRFVVL 558
Qy 354 QCP---AYFLQDFCGCEVALDWMEDFSLCREGQREWV-----IQIHESQFIIVVCSGKMK 406
Db 559 RCFWDSPPFIKSDGKQVASFALFD--KLRRREGGEMIEVIDLSKTYRNQV---KGIN 612
Qy 407 YFVDKKNYKHKGGRSGKGLFLVAVSAI-----AEKLQAKQSSAALSX 453
Db 613 MFTEKGEVMVLLGPNAGAKSTTMISSLIQPTSGDVLIKGSHKSKAIRSILGVVPO 672
Qy 454 FIAYFYSCB-----GDVPGILDSTKYRLMDNLPLQCLSHLHSDHGLQFPQGHOTRQ 507
Db 673 EIAYVHDLTARENLAFFGKIYGLKGEELKGR-MESTLQLV-----GLEE-----RQN 718
Qy 508 SRRNYFRSKGRSLYVAICNMHQ---FIDEEP 536
Db 719 DRVHTFGGKMKRLNIAVALLHEPELIIMDEP 750

RESULT 6
TI17212
hypothetical protein DKFZp434P211.1 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: TI17212
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
A;Accession: TI17212
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-488;489-535 <POU>
A;Cross-references: UNIPROT:Q9NTU6; EMBL:AL117401
A;Experimental source: adult testis; clone DKFZp434P211
A;Note: the cDNA sequence contains a -1 frameshift near codon 488
C;Genetics:
A;Note: DKFZp434P211.1

Query Match 2.9%; Score 110; DB 2; Length 535;
Best Local Similarity 23.5%; Pred. No. 1.3;
Matches 70; Conservative 42; Mismatches 108; Indels 78; Gaps 17;

Qy 439 KLRQAKQSS-SAALSXKFTAVFYDVSCEGDVPGI-----LDLSKTYRLMDNLPO 485
Db 103 RYNQTSQTSWTSSCTNRNAISSSYSTGGLFGLKRRRGFPASSHCQLTSSSKTVSEDRPQ 162

Db 747 IFSTANPEWNNVNSREINTITRVEDEELDDIDDHHPNQOQKPKQGLSGL 806
Qy 566 ----VLNDVMCKPGPESDFCLKVEAAVLGATGPADSHQESQHGL-----DQ 608
Db 807 SKQKMAARFNSFKGLKQMAAKNEKSVV-----TNDKEHEKNGATVQIKKKYFTSSDE 862
Qy 609 DGEARPALDGSAAQLPLLHTVKAGSPSDMPRDSGIDYSSVPSSELSPLMEGLSTDOTET 668
Db 863 MGAAKMA-----QSKLOD-----NLKKLGISLRITEM 890
Qy 669 SSLTESVSSSS 679
Db 891 EDTAKSFSTA 901
RESULT 9
S37627
protein-tyrosine kinase (EC 2.7.1.112), receptor-type - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S37627
R;Boehm, B.; Holtrich, U.; Wolf, G.; Luzius, H.; Grzeschik, K.H.; Strehhardt, K.; Ruebs
Oncogene 8, 2857-2862, 1993
A:Title: PCR mediated detection of a new human receptor-tyrosine-kinase, HEK 2.
A:Reference number: S37627; MUID:93390963; PMID:8397371
A:Accession: S37627
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-998 <BO>
A:Cross-references: UNIPROT:P54753; EMBL:X75208; NID:G406867; PIDN:CAA53021.1; PID:G4068
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein ki
F:631-899/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:922-988/Domain: SAM homology <SAM>
Query Match 2.8%; Score 109; DB 2; Length 998;
Best Local Similarity 18.9%; Pred. No. 3.9; Mismatches 301; Indels 250; Gaps 42;
Matches 157; Conservative 122;
Qy 1 ADTCGWRMKAARPLC-----VANEGVGPA-----SRNSG-----LYNITPKY 39
Db 268 ACTCATGHEPAKESQCRPCPPGSKYKAGQEGPCLPCPPNSRTTSPAASICTCHNNFYRA 327
Qy 40 DN-----CTTLPNVGKHVIADAQNTISQYACHDQVAVTILMS-PCALGIEFLKGRV 92
Db 328 DSDSADSACTTVPSP-PRGVISNV-----NETSLILEWSEPRDLGVRDLDLYNV 375
Qy 93 ILEELKSEG-----RQCOOLILKDPKOLNSSPKRTGMESQPLNKKFETDYFVKVPPPS 147
Db 376 ICKKHGAGGASACSRCDNDVEFVPRQLGLSEPRVHTS-----HLAHTRYTFEQVANG 430
Qy 148 IKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHGSDMQVSDFHAPHNFGFR 207
Db 431 VSGKSPLPRPYAAVNITNQAPSEV-----PTLHSSSGSLTISWAPPERPNG-- 481
Qy 208 FFYLHYLKHGEPF-KRKCTCKQEQTTTSCLLQNVSP-GDYIIELVDDTNTTRKVMHYA 265
Db 482 -VILDYEMKY---PEKSGIASTVTSQMSVQLDGLRDPDARVYVQV-----RARTVAGY 532
Qy 266 -LKPVH---SPWAGPIRAVAITVPLVVISAFATL-----FTVMCRKQOENIYSH 311
Db 533 QYSRPAEFETTTSERSGAQQLQEQPLIVGSAAGLVFVAVVIAIVCLRKQRH----- 587
Qy 312 LDEESSESTYTAALPRELRPRPVLCYSSKQGNHNVVQCFAYFLQDFC-CCEVAL 370
Db 588 -----GSQSEYTEKL-QQTIAPGMKVIIDPFTYEDPN--EAVREFAKVIDSCVKEIVI 639
Qy 371 DLWEDFSLCRGQREWVQKIHESOFIIVCVSKGMKYFYDKKNYKHGGGSGSGKGEFL 430
Db 640 GAGEGFEVCR-----GRLKQPGREVF- 661

Qy 431 VAVSAI-----AEKLROAKQSSAALSXPIAVFYFDYSCGDDVPGLDLS---TKYR----- 478
Db 662 VAIKTLKVGVTQRQRDFLSEASIMQGF-----DHPNIIRLEGGVVTKSRPVMI 710
Qy 479 --LMDNLPOLCSHLHSDHGLQEBQHT-----RQGSRRNT-FRSKSGRS 520
Db 711 TEFMENC-ALDSFURLND-----GQFTVQLQVLMRLGIAAGMKYLSBMNTVHRDLAARN 763
Qy 521 LYV---AIC-----NMHQFIDEEDPWFEPKQVPFPHPP-----PLRYREP---VLEKFPDS 563
Db 764 ILVNSNLVKVSDFGLSRFLDDPS-----DPTYTSSLGCKIPIRMTAPEAIAVRKFTS 817
Qy 564 -----GLVLDVMCKPGPESDFCLKVEAAVLGATGPADSHQESQHGLDQGEARPAL 616
Db 818 ASDVMSYGIWMEVMS-----YGERPYWDMNSQDVINAVEQDYRLPPEM 861
Qy 617 DGSAAQLPLLHTVKAGSPSDMPRDSGLYDS-----SVPSSELSPLMEGLS 662
Db 862 DCPTALHQLMLDCWVRDRNLRPKFSQIVNTLQKLRNAASLKVIASAQSGMSQPLDRTV 921
Qy 663 TDQTETSLTESVSSSGLGEBEPPALPSKLSLSSGCKADLGCRSYTDEL 712
Db 922 PDYITFTVGDWLDAIK-MGRYK-----ESFVSAGFASFDLVAQWTAEDL 965
RESULT 10
149071
protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149071
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A:Title: Identification of novel protein kinases expressed in the myocardium of the deve
A:Reference number: 149071; MUID:95200798; PMID:7893599
A:Accession: 149071
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-938 <RES>
A:Cross-references: UNIPROT:Q60669; EMBL:U11493; NID:G595418; PIDN:AAA67925.1; PID:G5954
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
F:571-839/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif
F:862-928/Domain: SAM homology <SAM>
Query Match 2.8%; Score 107.5; DB 2; Length 938;
Best Local Similarity 19.3%; Pred. No. 4.7;
Matches 152; Conservative 115; Mismatches 271; Indels 251; Gaps 42;
Qy 1 ADTCGWRMKAARPLC-----VANEGVGPA-----SRNSG-----LYNITPKY 39
Db 205 ACTCATGHEPAKESQCRPCPPGSKYKAGQEGPCLPCPPNSRTTSPAASICTCHNNFYRA 264
Qy 40 DN-----CTTLPNVGKHVIADAQNTISQYACHDQVAVTILMS-PCALGIEFLKGRV 92
Db 265 DSDSADSACTTVPSP-PRGVISNV-----NETSLILEWSEPRDLGVRDLDLYNV 312
Qy 93 ILEELK-SEG-----RQCOOLILKDPKOLNSSPKRTGMESQPLNKKFETDYFVKVVP 144
Db 313 ICKKRGSSGAGGAPATCSRCDNDVEFVPRQLGLTERRVHIS-----HLAHTRYTFEQVA 367
Qy 145 FPSIKNESNYHPFFRTRACDLLQPDNLACKPFWKPRNLNISQHGSDMQVSDFHAPHNF 204
Db 368 VNGVSGKSPLPRPYAAVNITNQAPSEV-----PTLHSHSTSGSLTISWAPPERPN 420
Qy 205 GFRFFYLHYLKHGEPF-KRKCTCKQEQTTTSCLLQNVSP-GDYIIELVDDTNTTRKY- 261
Db 421 G---VILDYEMKY---FEKSKAIASTVTSQMSVQLDGLQDPDARVYVQV-----RARTVA 469
Qy 262 -----MHYALKPVHSPWAGPIRAVAITVPLVVISAFSA-----TLFTVMCRKQOENI 308
Db 470 GYGQYTHPAEFETTTSERSGAQQLQEQPLIVGSAAGLVFVAVVIAIVCLRKQRH--- 527


```
Qy 576 PESDFCLKVEAAVLGATGPADSOHESQHG-----GLDQDG-----EARP- 614
Db 3644 PGRH-----TSAKEHRHSDIGRHSGRHAGEPGRRAAKPHARDWGRHEARPH 3691
Qy 615 -----ADGSAALOPLHTV 629
Db 3692 PQASPAPAMQKQGPYPSSADYSQSRAPSAVHHASEKSGRQAHTGPSALQPKADTQ 3751
Qy 630 KAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDTOTETSLTSVSSSSGLGEEPPAL 689
Db 3752 AQPQWGRQAAPGQSQPPSSROT-----PSGTASGRPQTQOQOQOQOQOGLGQAQQA 3808
Qy 690 PSK 692
Db 3809 PSQ 3811

RESULT 13
Protein F1504.27 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86477
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86477
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-638 <STO>
A:Cross-references: UNIPROT:Q9LQF8; GB:AE005172; NID:98778345; PIDN:AAF79353.1; GSPDB:GN
C:Genetics:
A:Gene: F1504.27
A:Map position: 1

Query Match 2.8%; Score 106.5; DB 2; Length 638;
Best Local Similarity 19.4%; Pred. No. 3.2;
Matches 94; Conservative 63; Mismatches 175; Indels 153; Gaps 24;

Qy 59 NITISQVACHDQVAVTILWSPGALGIEFLKGRPRVILELKSREGQCQQLILKDPKQLNS 118
Db 275 DIKYQYISCHLQDCFYVHS-----KCATHEENVWDGKELEWIESDETEDISP 322
Qy 119 FKRTGMESQPFNLMMKFETDYFKVVPFP-----SIKNESNYHPFFFTTRACDLLLLQPDNLAC 175
Db 323 FENLG-----DGFIKHCFKHRLKLNKHDGARDTEKQCRAC---IYF--IVS 364
Qy 176 KPFKPRNLNLSQHG--SDMQVSPFHAPHNFGFRFYLYHLKHEGP--FKRKTCKQEQT 231
Db 365 HQFYHCKKCNYSLEHVCAGLSKLDHALN-----HTLSPSPGKFCSCSREST 416
Qy 232 TETTSCLLQNVSPGDIYIELVDVDTNTRKVMHYALKPVHS PWAGPIRAVAITVPLWISA 291
Db 417 GFSYIC--SNKGCQDFVLVDV-----RCISVLYBFYHRSHEH-----PIFIST 457
Qy 292 FATLFTVMCRKKQENIYSHLDEESE--SSTYTA--LPRE----RLRPRPKVFLCYSSKDG 346
Db 458 YNSKDEILCKVCKKCLGNHLOCTICEFTMCSALIPDEIHVKFDKHLTLSCGESAD- 516
Qy 347 QNHMNVQCFAYFLQDFQCGCEVALDWEDFSICREGREWIOKTHESQFIIVVCSKGMK 406
Db 517 ----NTYCEV-----CEQLDPKEWFTCNK-----CCITIH-----LHCIFGSS 553
Qy 407 YFVDKKNYKHGGGRSGKGEFLIVAVSAIAEKLQAKQSSAALSKFIAYFYDYSCEGD 466
```

```
Db 554 VFM-----KPG-----SIFRDYGVKQV 570
Qy 467 VPGILDLSKYRLMDNLPQLCSHLHSRDHGLQEPGQHTROGSRN--YFRSKSGRSY-V 523
Db 571 V-----FRNSNTRQLCYMCHNCTGL-----IFYEGYRRNATYYVYHNSNRSTRM 616
Qy 524 AICNM 528
Db 617 IFCSL 621

RESULT 14
T30851
lysosomal trafficking regulator, long splice form - mouse
N:Alternate names: beige protein homolog
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30851
R:Barbosa, M.D.F.S.; Tchernev, V.T.; Kingmore, S.F.
submitted to the EMBL Data Library, September 1996
A:Description: Two bg or not two bg? Longest isoform of mouse Lysat (beige) gene.
A:Reference number: Z20903
A:Accession: T30851
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3788 <BAR>
A:Cross-references: UNIPROT:P97412; EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC530
A:Experimental source: strain C57BL/6J
C:Genetics:
A:Gene: Lysat
A:Map position: 1
C:Keywords: alternative splicing

Query Match 2.8%; Score 106; DB 2; Length 3788;
Best Local Similarity 19.6%; Pred. No. 49;
Matches 154; Conservative 99; Mismatches 275; Indels 256; Gaps 44;

Qy 16 LCVANEGVGPA-----RNSGLYNIITFKYDNCCTTYLNPVKGHVIAQAQNTIT 62
Db 658 LC-----GAGPTISGLPSPSYRFQGIPLSSGSEDLWKWDALEYQSFVQE--DRLHNIQI 711
Qy 63 SOYACH--DQVAVTILWSPGALGIEFLKGRFVILELSEKSEG-----RQCCQLIKDPKQLN 116
Db 712 ANHICNLLOKGNVVVQW-----KLYNYIFNPVLQGVGVVHHCQQLSIPS----- 756
Qy 117 SSFKRTGMESQPFNLMMKFET--DYFKVVP-----FPSIKN-----ESNY----- 154
Db 757 ---AQTHMCSQLKQYLPQEVLIQYIKTLFVLKSRVIRDLFLSCNGVNHIELNYLDGIR 813
Qy 155 -HPF-FPRTRACDLLLLQPDNLACKPFWKPRNLNISQHGSDMQVSPDHAPHNFGFRFFYLH 212
Db 814 SHSLKAFETLIVSAGEQKDAVLVDV---DGLDIQQLPFLSV----- 853
Qy 213 YKLKHEGPFKRKTCKEQETTETTSCLLQNVSPGDIYIELVDVDTNTRKVMHYALKPVHSP 272
Db 854 -----GFLSK-----QQASSDPCSLRK-----FYASLRPDPKPKRTIHH---QDVH-- 893
Qy 273 WAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEESESESTYTAALPRERLR 332
Db 894 -----INTINFLCVAF-----LCVSKEADS-----DRESANESEDTSGYDPSPPSE 934
Qy 333 PRPKVFLCYSSKQGNHNVV---OCFAYFLQDFQCGCEVALDWEDFSICREGREWV- 387
Db 935 PLSHMLPCLSLIED-----VVLPSPECLHH-----AADIW---SMCR-----WLY 970
Qy 388 -IQKHESQFI-----IVVCSKGMKYFVDKKNYKHGGGRSGKGEFL-----LVAVSAI 436
Db 971 MINSVFQKQFIRLGGFQVCHB-LIFMIIQKLFRSHTEDQGRRGQSGMSENENQELIRIS-- 1027
Qy 437 AEKLQAKQSSAALSKFIAYFYDYSCEGDVPGIL--DLSTKYRLMDN-----LPQ 485
Db 1028 -----YPELTLKGDVSSATAPDLGFLRKSADSVRGFSQSPVLPT 1066
```

Qy 486 LCSHLHRDHGLQEPGQHTROGSRNRYFRSKGRSLYVAICNMHQFIDERPDPFEKQFVP 545
Db 1067 SAEQIVATE---SVPGE-----RKAFMSQOSETLSQIRLLESLLD-----IC 1106
Qy 546 FHPPPLRYRPREVLEKFDGLVINDVMCK-----PCPESDFCLKVEAAVLG 590
Db 1107 LHSARACQKWELELPQGLSVENICELREHLSQSKVAETELAKPLFDALLRVALGNHS 1166
Qy 591 A-TGPADS-----QHESQHGGLDQGEARPALDGSAAOPLLHTVKAGSPSDM---PRDSG 642
Db 1167 ADLGFDAVTEKSHPSSEBLLSQPCDFSEEAEDSQCCSLKLLGEEGVEADSESNPEDVD 1226
Qy 643 IYDSSVPSSELSLPLMEGLSTDQETSSLTSTSVSSSSGLGE---EPPALPSKLLSSGSC 699
Db 1227 TODDGV---ELN-PEAEGFS-GSIVSNNLLENLTH---GEIYYEICMLGMLNLLLSAKA 1277
Qy 700 KADL 703
Db 1278 KLDV 1281
RESULT 15
JC6093
dead ringer nuclear protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: JC6093
Mol. Cell. Biol. 16, 792-799, 1996
R;Gregory, S.L.; Kortschak, R.D.; Kallionis, B.; Saint, R.
A;Title: Characterization of the dead ringer gene identifies a novel, highly conserved f
A;Reference number: JC6093; MUID:96182081; PMID:8622680
A;Accession: JC6093
A;Molecule type: mRNA
A;Residues: 1-301 <GRE>
A;Cross-references: UNIPROT:Q24573; GB:U62542; NID:g1480739; PIDN:AAB05771.1; PID:g14807
A;Experimental source: embryo
C;Genetics:
A;Gene: dri
C;Keywords: DNA binding; embryo

Query Match 2.7%; Score 105; DB 2; Length 901;
Best Local Similarity 20.4%; Pred. No. 7,1;
Matches 96; Conservative 56; Mismatches 157; Indels 162; Gaps 23;
Qy 370 LDLWEDFSL--CREG-----OREW--VIQIHESQFI-----IVVCSKGMKYF---VDK 411
Db 313 LDLYELNVIARGLVVDVINKLWQEIIGKHLPLSSITSAFTLRTQYMKLYPYCEK 372
Qy 412 KNYK-----HKGGRGSGKE-----LFLVAV 433
Db 373 KNLSTPAELQAIQGNREGRRSSYGQYEAHMNQMPPISRPSLPGMQQMSPLALVTH 432
Qy 434 SAIAEKLK-QAKOSSAALSFIAYFDYSCGDPVPGIGLDLSTKYRLMDNLPQLC----- 487
Db 433 AAVANNQQAQAAAAAAHRLMGA---PAFGQPNLVKQEIERSMWEYL-QLIQAKKE 487
Qy 488 -----SHLGRDHGLQEPGQH-----TRQGSRRNYFRSKGR-----SL 521
Db 488 QGMPPVLGGNHPHQOQHSQQOQHHQOQQOQQOQQHLLQOQRQSQSPDLSKHEALSA 547
Qy 522 YVAICNMHQ-----FIDEEDPWFQKVPFHPPL-----RYREPVLKFD----- 562
Db 548 QVALWHMHNNSPPGSAHTSPQOREALNLSDSPPLNLTNIKREREREPTPEVDQDKFV 607
Qy 563 -----SGLVINDVMCKPGESDFCLKVE--AAVLGATPADSOHESQHGGLDQDG 610
Db 608 QOPPAKEVGSGLL-----PPGFPANFYLNPHNMAVAAGAAG---FHHPSMGHQDDAAS 658
Qy 611 BARPALDGSAAQLPLLHTVTKAGSPSDMPRDSGIYDSSVPSSELSLPLMEG----- 660
Db 659 EGEPEDD-----YAHGEHNTTGNSSSMHDDSEFQO-----MNGHHHHTHLLD 701

Qy 661 LSTDQTETSSLTSTSVSSSSGLGEEPPALPSKLLSSGSCKADLGCRSYTDE 711
Db 702 KSDDSAIENSPTTSTTTTGGSGVGRHSSPVSTK--KKGAKPQSGGKDLPT 750
Search completed: August 9, 2005, 11:49:57
Job time : 31.7981 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2005, 11:36:31 ; Search time 113.24 Seconds
(without alignments)
3246.847 Million cell updates/sec

Title: US-10-717-282-2_COPY_36_753

Perfect score: 3829

Sequence: 1 ADTCGRMKAAARPRLCVAN.....CKADLGRSYTDELHVAAPL 718

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|---------------------|
| 1 | 3735 | 97.5 | 739 | 2 Q8NFS0 | Q8nfs0 homo sapien |
| 2 | 3731 | 97.4 | 739 | 2 Q8NFM7 | Q8nfm7 homo sapien |
| 3 | 3708 | 96.8 | 707 | 2 Q8RVF4 | Q8rvf4 homo sapien |
| 4 | 3703 | 96.7 | 728 | 2 Q6UW15 | Q6uw15 homo sapien |
| 5 | 3222.5 | 84.2 | 738 | 2 Q8UJZL1 | Q8ujz1 mus musculus |
| 6 | 3170 | 82.8 | 595 | 2 Q8N113 | Q8n113 homo sapien |
| 7 | 3005 | 78.5 | 564 | 2 Q9UFA0 | Q9ufa0 homo sapien |
| 8 | 2844 | 74.3 | 741 | 2 Q7T2L7 | Q7t2l7 gallus gall |
| 9 | 2834 | 74.0 | 697 | 2 Q8AV76 | Q8av76 gallus gall |
| 10 | 2675.5 | 69.9 | 594 | 2 Q8K447 | Q8k447 mus musculus |
| 11 | 2616.5 | 68.3 | 582 | 2 Q8R5J8 | Q8r5j8 mus musculus |
| 12 | 1950.5 | 50.9 | 745 | 2 Q8QHJ9 | Q8qhj9 brachydanio |
| 13 | 1941.5 | 50.7 | 745 | 2 Q8QHJ6 | Q8qhj6 brachydanio |
| 14 | 354 | 9.2 | 109 | 2 Q8HXE8 | Q8hxe8 macaca fasc |
| 15 | 310 | 8.1 | 866 | 1 I17R_HUMAN | Q8f46 homo sapien |
| 16 | 306 | 8.0 | 864 | 1 I17R_MOUSE | Q60943 mus musculus |
| 17 | 205 | 5.4 | 769 | 2 Q69HQ3 | Q69hq3 ciona intes |
| 18 | 170.5 | 4.5 | 846 | 2 Q9NA64 | Q9na64 caenorhabdi |
| 19 | 135.5 | 3.5 | 502 | 1 I17S_HUMAN | Q9nrm6 homo sapien |
| 20 | 126.5 | 3.3 | 718 | 1 YS02_CAEEL | Q10128 caenorhabdi |
| 21 | 121 | 3.2 | 993 | 2 Q7PW55 | Q7pw55 anopheles g |
| 22 | 117.5 | 3.1 | 562 | 2 Q93755 | Q93755 homo sapien |
| 23 | 117 | 3.1 | 757 | 2 Q13399 | Q13399 utillago ma |
| 24 | 116.5 | 3.0 | 637 | 2 Q6AZ51 | Q6az51 rattus norv |
| 25 | 116.5 | 3.0 | 901 | 2 Q9KE04 | Q9ke04 bacillus ha |
| 26 | 116 | 3.0 | 4736 | 2 Q7YT99 | Q7yt99 mytilus gal |
| 27 | 115 | 3.0 | 859 | 1 MR1P_HUMAN | Q8nfw9 homo sapien |
| 28 | 113.5 | 3.0 | 617 | 2 Q8K4C1 | Q8k4c1 mus musculus |
| 29 | 113.5 | 3.0 | 1190 | 2 Q6H470 | Q6h470 oryza sativ |
| 30 | 112.5 | 2.9 | 549 | 2 Q99754 | Q99754 homo sapien |
| 31 | 112.5 | 2.9 | 783 | 2 Q6FJR3 | Q6fjr3 candida gla |

| | | | | | |
|----|-------|-----|------|--------------|---------------------|
| 32 | 112.5 | 2.9 | 1685 | 2 Q6H969 | Q6h969 homo sapien |
| 33 | 112.5 | 2.9 | 1685 | 2 Q6ZU00 | Q6zuu0 homo sapien |
| 34 | 111.5 | 2.9 | 370 | 2 Q8N2R7 | Q8n2r7 homo sapien |
| 35 | 111.5 | 2.9 | 370 | 2 Q96KN9 | Q96kn9 homo sapien |
| 36 | 111.5 | 2.9 | 862 | 2 Q6NUK8 | Q6nuk8 homo sapien |
| 37 | 111 | 2.9 | 592 | 2 Q6CED7 | Q6ced7 varrowia li |
| 38 | 110.5 | 2.9 | 499 | 1 I17S_MOUSE | Q9jip3 mus musculus |
| 39 | 110.5 | 2.9 | 805 | 2 Q758M4 | Q758m4 ashbya gos |
| 40 | 110.5 | 2.9 | 1433 | 2 Q6PFW1 | Q6pfw1 homo sapien |
| 41 | 110 | 2.9 | 428 | 2 Q9NTU6 | Q9ntu6 homo sapien |
| 42 | 110 | 2.9 | 592 | 1 STB3_MOUSE | Q60770 mus musculus |
| 43 | 110 | 2.9 | 618 | 2 Q6DE54 | Q6de54 xenopus lae |
| 44 | 110 | 2.9 | 917 | 2 Q81789 | Q81789 arabidopsis |
| 45 | 109.5 | 2.9 | 764 | 2 Q6NU08 | Q6nu08 xenopus lae |

ALIGNMENTS

RESULT 1

| | | | | |
|----|---|--------------|------|---------|
| ID | Q8NFS0 | PRELIMINARY; | PRT; | 739 AA. |
| AC | Q8NFS0; | | | |
| DT | 01-OCT-2002 (Tremblrel. 22, Created) | | | |
| DT | 01-OCT-2002 (Tremblrel. 22, Last sequence update) | | | |
| DT | 01-MAR-2004 (Tremblrel. 26, Last annotation update) | | | |
| DE | IL-17RD. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Gilbert J.M., Gorman D.M.; | | | |
| RL | Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AF458067; AAM7751.1; -. | | | |
| DR | GO; GO:0016020; C:membrane; IEA. | | | |
| DR | GO; GO:0004888; F:transmembrane receptor activity; IEA. | | | |
| DR | InterPro; IPR000157; TIR. | | | |
| SQ | SEQUENCE 739 AA; 82440 MW; 1670803DDC0DF17 CRC64; | | | |

Query Match 97.5%; Score 3735; DB 2; Length 739;

Best Local Similarity 97.9%; Pred. No. 7.8e-275;

Matches 703; Conservative 0; Mismatches 1; Indels 14; Gaps 1;

| | | | |
|----|-----|--|-----|
| Qy | 1 | ADTCGRMKAAARPRLCVANEGVGPASRNSGLNITFKYDNCCTTYLNPVGHVIADAQNI | 60 |
| Db | 36 | ADTCGRMKAAARPRLCVANEGVGPASRNSGLNITFKYDNCCTTYLNPVGHVIADAQNI | 81 |
| Qy | 61 | TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCQQLIKDPKQLNSFPK | 120 |
| Db | 82 | TISQVACHDQVAVTILMSPGALGIEFLKGFVRVILEELKSEGRQCQQLIKDPKQLNSFPK | 141 |
| Qy | 121 | RTGMESQFLNKKETDFTVVKVPPSPISKNSNTHPPFPFRTRACDLILQPNLACKPFWK | 180 |
| Db | 142 | RTGMESQFLNKKETDFTVVKVPPSPISKNSNTHPPFPFRTRACDLILQPNLACKPFWK | 201 |
| Qy | 181 | PRNLNISQSGSDMQVSDPHAPNHFGRFFYLHYLKHGPPFKRTCKQEQITTEMTSCLLQ | 240 |
| Db | 202 | PRNLNISQSGSDMQVSDPHAPNHFGRFFYLHYLKHGPPFKRTCKQEQITTEMTSCLLQ | 261 |
| Qy | 241 | NVSPGDYIIELVDNTTRKVMHVALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC | 300 |
| Db | 262 | NVSPGDYIIELVDNTTRKVMHVALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC | 321 |
| Qy | 301 | RKQKQENTYSHLDESSSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNMVQCFAFPL | 360 |
| Db | 322 | RKQKQENTYSHLDESSSSSTYTAALPRERLRPRPKVFLCYSSKQGNHNMVQCFAFPL | 381 |
| Qy | 361 | QDFCGCEVALDLWEDFSLCRGQREWVTKTHESQFIIVVCSKGMKYFVDKKNYKHGGG | 420 |
| Db | 382 | QDFCGCEVALDLWEDFSLCRGQREWVTKTHESQFIIVVCSKGMKYFVDKKNYKHGGG | 441 |

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Qy 421 RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCRGDVPGLDLSKTYRLM 480
Db |||||
Qy 442 RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCRGDVPGLDLSKTYRLM 501
Db |||||
Qy 481 DNLPLQCSHLHSRDHGLQEPQGHTRQGSRRNYFRSKSGRSLYVAICNNHOFIDEEPWF 540
Db DNLPLQCSHLHSRDHGLQEPQGHTRQGSRRNYFRSKSGRSLYVAICNNHOFIDEEPWF 561
Qy 541 KQFVFPFPPPLRYREPVLKFDPSGLVLDVNCVKPGPESDFCLKVEAAVLGATGADSOHE 600
Db |||||
Qy 562 KQFVFPFPPPLRYREPVLKFDPSGLVLDVNCVKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy 601 SOHGGLDQGEARPALDGSAAQLPLLHTVKAGSPDMPRDSGIYDSSVPSELSPLMWEG 660
Db SOHGGLDQGEARPALDGSAAQLPLLHTVKAGSPDMPRDSGIYDSSVPSELSPLMWEG 681
Qy 661 LSTDQTTSSLTSESVSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAPL 718
Db LSTDQTTSSLTSESVSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAPL 739

RESULT 2
Q8NFM7 PRELIMINARY; PRT; 739 AA.
AC O8NFM7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein long form.
GN Name=IL17RLM;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S.Q., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "hsf inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
RA Chen Y., Liu L., Fu X.Y., Chang Z.J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF494208; AAM74077.1; -
DR Genew; HGNC:17616; IL17RD
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Receptor.
SQ SEQUENCE 739 AA; 82441 MW; BCDA2A95261B0277 CRC64;

Query Match 97.4%; Score 3731; DB 2; Length 739;
Best Local Similarity 97.8%; Pred. No. 1.6e-274;
Matches 702; Conservative 1; Mismatches 1; Indels 14; Gaps 1;

Qy 1 ADTCGRWKAARPRCLCVANEGVGPASRNSGLYNITFKYDNCCTTLYNPVGKHVIADAQNI 60
Db 36 ADTCGRW-----GVGPASRNSGLYNITFKYDNCCTTLYNPVGKHVIADAQNI 81

Qy 61 TISYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSGFX 120
Db 82 TISYACHDQAVATILWSPGALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSGFX 141

Qy 121 RTGMSQPLNMKFTDYFVKVVPFPPSIKNESNTHPPFTRACDILLQPNLACKPFWK 180
Db 142 RTGMSQPLNMKFTDYFVKVVPFPPSIKNESNTHPPFTRACDILLQPNLACKPFWK 201

Qy 191 PRNLNISQHSQDMQVSPDHAPHNFRFFYLHYLKLKHEGPFKRKTCRQEQTTETSCLLQ 240

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Db 202 PRNLNISQHSQDMQVSPDHAPHNFRFFYLHYLKLKHEGPFKRKTCRQEQTTETSCLLQ 261
Qy 241 NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
Db NVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
Qy 301 RKQQENIYSHLDEESSESYTAALPRERLRPRPKVFLCYSSKDGQNHNNVQCFAYFL 360
Db RKQQENIYSHLDEESSESYTAALPRERLRPRPKVFLCYSSKDGQNHNNVQCFAYFL 381
Qy 361 QDFCGCEVALDLMEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 420
Db QDFCGCEVALDLMEDFSLCREGQREWIQKIHESQFIIVVCSKGMKYFVDKKNYKHKGG 441
Qy 421 RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCRGDVPGLDLSKTYRLM 480
Db RSGKGELFLVAVSAIAEKLROAKOSSAALSKEFIAYVFDYSCRGDVPGLDLSKTYRLM 501
Qy 481 DNLPLQCSHLHSRDHGLQEPQGHTRQGSRRNYFRSKSGRSLYVAICNNHOFIDEEPWF 540
Db DNLPLQCSHLHSRDHGLQEPQGHTRQGSRRNYFRSKSGRSLYVAICNNHOFIDEEPWF 561
Qy 541 KQFVFPFPPPLRYREPVLKFDPSGLVLDVNCVKPGPESDFCLKVEAAVLGATGADSOHE 600
Db KQFVFPFPPPLRYREPVLKFDPSGLVLDVNCVKPGPESDFCLKVEAAVLGATGADSOHE 621
Qy 601 SOHGGLDQGEARPALDGSAAQLPLLHTVKAGSPDMPRDSGIYDSSVPSELSPLMWEG 660
Db SOHGGLDQGEARPALDGSAAQLPLLHTVKAGSPDMPRDSGIYDSSVPSELSPLMWEG 681
Qy 661 LSTDQTTSSLTSESVSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAPL 718
Db LSTDQTTSSLTSESVSSSGLGEEPPALPSKLLSSGCKADLCGRSYTDELHAVAPL 739

RESULT 3
Q6RVF4 PRELIMINARY; PRT; 707 AA.
AC Q6RVF4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SEF splice variant b.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testes;
RX PubMed=14742870; DOI=10.1073/pnas.0307952100;
RA Preger E., Ziv I., Shabtay A., Sher I., Tsang M., Dawid I.B.,
RA Altuvia Y., Ron D.;
RT "Alternative splicing generates an isoform of the human Sef gene with
RT altered subcellular localization and specificity.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:1229-1234(2004).
DR EMBL; AY489047; AAS15051.2; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 707 AA; 79493 MW; 7D3BE21EE038F17E CRC64;

Query Match 96.8%; Score 3708; DB 2; Length 707;
Best Local Similarity 99.7%; Pred. No. 8.2e-273;
Matches 696; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 21 EGVGPASRNSGLYNITFKYDNCCTTLYNPVGKHVIADAQNIISQYACHDQAVATILWSPG 80
Db 10 QGVGPASRNSGLYNITFKYDNCCTTLYNPVGKHVIADAQNIISQYACHDQAVATILWSPG 69

Qy 81 ALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSGFXKRTGMSQPLNMKFTDYFV 140
Db 70 ALGIEFLKGFVRVILEELKSEGRQCOQLILKDPKQNSGFXKRTGMSQPLNMKFTDYFV 129

```


OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21959295; PubMed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
RX Lin W., Furthauer M., Thiesse B., Thiesse C., Jing N., Ang S.-L.;
RT "Cloning of the mouse Sef gene and comparative analysis of its
RL expression with Fgf8 and Spry2 during embryogenesis.";
RL Mech. Dev. 113:163-168(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "Sef inhibits PC-12 cell differentiation by interfering with Ras-
RL mitogen-activated protein kinase MAPK signaling.";
RN J. Biol. Chem. 278:50273-50282(2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
RA Chen Y., Liu L., Fu X.Y., Chang Z.J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF459444; AAM28441.1; -;
DR EMBL; AF494210; AAM74079.1; -;
DR MGD; MGI:2159727; Il17rd.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 738 AA; 82347 MW; D8CE56230E3B8226 CRC64;

Query Match 84.2%; Score 3222.5; DB 2; Length 738;
Best Local Similarity 84.9%; Pred. No. 6.8e-236;
Matches 612; Conservative 37; Mismatches 51; Indels 21; Gaps 5;

QY 1 ADTCGWRKMAAARPLCVANEGVGPASRNSGLYNTFKYDNCCTYLPVGVGHVIADAQNI 60
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 81
QY 61 TISQYACHDQVAVTILWSPGALGIEFLKGRFVILEELKSEGRQCQQLILKDPKQLNSFFK 120
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 141
QY 121 RTGMESQPFLLNMKPEFDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWK 180
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 201
QY 142 RTGMESQPFLLNMKPEFDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWK 201
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 240
QY 181 PRNLNISOHSDMVOVSFDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTTSCLLQ 240
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 261
QY 202 PRNLNISOHSDMVOVSFDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTTSCLLQ 261
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 300
QY 241 NVSPGDYIIELVDNTTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMC 300
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 321
QY 262 NVSPGDYIIELVDNTTNTTRKAAQYVVKSVQSPWAGPIRAVAITVPLVVISAFATLFTVMC 321
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 360
QY 301 RKQQENIYSHLDESSESSTYTAALPRERLRPRPKVFLCYSGDKGQNHMVVOCFAYFL 360
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 381
QY 322 RKQQENIYSHLDESSESSTYTAALPRERLRPRPKVFLCYSGDKGQNHMVVOCFAYFL 381
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 420
QY 361 QDFCGCEVALDLWEDFSICREGQREWAIQKHESQFIIVVCSKGMKYFVDKKNYKHGGG 420
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 441
QY 382 QDFCGCEVALDLWEDFSICREGQREWAIQKHESQFIIVVCSKGMKYFVDKKNYKHGGG 441
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 480
QY 421 RGSQKGLFLVAVGAIKFLQAKQSSAALSKFIIVFYDYSCEGDVPGIIDLSTKYRLM 480
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 501
QY 442 RGAQGEFFLVAVAAIEKFLQAKQSSAALSKFIIVFYDYSCEGDVPGIIDLSTKYRLM 501
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 539
QY 481 DNLPLQCSHLHSDHGLQEP-CQHTROGSRNFRSKSGSLYVAICNMHQFIDEEPDWF 539
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 558
QY 540 EKQFVFPHPPLRYRPRVLEKFGSLVNDVMCKPGPESDFCLKVEAAVLGATGPADSOH 599
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 618
QY 559 EKQFIPFHPVRYQRPVLEKFGSLVNDVSKPGPESDFCKKVEACVLGAAGPADSYS 618
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 657
QY 600 --ESQHGGLDQDGEARPALDGSAAQLPQLLHTVKAQSPSDMPRDSGIYDSSVPSSELSLPL 657
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 678
QY 619 YLESQHVGLDQDTEAQPSCDAPALQPLLHAVKAGSPSEMPRDSGIYDSSVPSSELSLPL 678
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 717
QY 658 MEGSLTDQDTSTSLTSSVSSSSGLGEBEPPALSKLLSSGCKADLCRCGYTDELHVAAP 717
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 737
QY 679 MEGSLPDQITSTSLTSSVSSSSGLGEBEDPPLFSLKLLASGVSR-EGCHSHTEDELQALAP 737
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 718 L 718
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 738 L 738

RESULT 6
Q8N113
ID Q8N113 PRELIMINARY; PRT; 595 AA.
AC Q8N113;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 17 receptor-like protein short form (Hypothetical protein
DN DKFZP434L0320).
GN Name=IL17RLM; Synonyms=DKFZP434L0320;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "Sef inhibits PC-12 cell differentiation by interfering with Ras-
RL mitogen-activated protein kinase MAPK signaling.";
RN J. Biol. Chem. 278:50273-50282(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Otenwaeider B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF494211; AAM74080.1; -;
DR EMBL; AL8333913; CAD38769.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Hypothetical protein; Receptor.
SQ SEQUENCE 595 AA; 66846 MW; 7E6BBB64F73B2112 CRC64;

Query Match 82.8%; Score 3170; DB 2; Length 595;
Best Local Similarity 99.8%; Pred. No. 4.9e-232;
Matches 594; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 124 MESQPFLLNMKPEFDYFVKVVPFPPSIKNESNYHPFFRTRACDLLLLQPDNLACKPFWKPRN 183
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 60
QY 184 LNLSQHSQSDMVSDHAPHNFGFRFFYLHYLKHGEPFKRKTCKOEQTTSCLLQNV 243
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 120
QY 244 PGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 303
DB |||||-----GVGPASRNSGLHNTFRYDNCCTYLPVGGKHAIDAAQNI 180
QY 121 PGDYIIELVDDTNTTRKVMHYALKPVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180

QY 304 QENIYSHLDDESSSTYTAALPRERLRPRKPVFLCYSSKGGQNMVWVQCFAIFLQDF 363
DB 181 QENIYSHLDDESSSTYTAALPRERLRPRKPVFLCYSSKGGQNMVWVQCFAIFLQDF 240
QY 364 CGCEVALDLWDFSLCREGQEWIWKIHESQFIIVVCSKGMKVFVDKKNYKHGGGRGS 423
DB 241 CGCEVALDLWDFSLCREGQEWIWKIHESQFIIVVCSKGMKVFVDKKNYKHGGGRGS 300
QY 424 KGEFLVAVSAIAEKLRQAKQSSAALSKEFIIVVCSKGMKVFVDKKNYKHGGGRGS 483
DB 301 KGEFLVAVSAIAEKLRQAKQSSAALSKEFIIVVCSKGMKVFVDKKNYKHGGGRGS 360
QY 484 POLCSHLHSRDHGLQEPQHTROGSRNRYFRSKGRSLYVAICNNHQFIDEEPWFKEQF 543
DB 361 POLCSHLHSRDHGLQEPQHTROGSRNRYFRSKGRSLYVAICNNHQFIDEEPWFKEQF 420
QY 544 VPFPPLRYREPVLKPDGSLVNDVMCKPGPSDFCLKVEAAVLGATGADSOHESQH 603
DB 421 VPFPPLRYREPVLKPDGSLVNDVMCKPGPSDFCLKVEAAVLGATGADSOHESQH 480
QY 604 GGLDODGEARPDALDGSAAALQPLHTTVKAGSPDMPRDSGIYDSSVPSSELSPLMEGLST 663
DB 481 GGLDODGEARPDALDGSAAALQPLHTTVKAGSPDMPRDSGIYDSSVPSSELSPLMEGLST 540
QY 664 DOTETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGRSYTDELHVAAPL 718
DB 541 DOTETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLGRSYTDELHVAAPL 595

RESULT 7

Q9UFAO PRELIMINARY; PRT; 564 AA.
ID Q9UFAO
AC Q9UFAO
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp434N1928 (Fragment).
GN Name=DKFZp434N1928;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Testis;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL133097; CAB61408.1; -
DR FIR; T42695; T42695.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523B88C CRC64;

Query Match 78.5%; Score 3005; DB 2; Length 564;
Best Local Similarity 99.8%; Pred. No. 1.6e-219;
Matches 563; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 155 HPFFRTRACDILLOPDNLACPKFVKPRNLINISQHGSDMVSFDPHAPNFGFRFFVLYHK 214
DB 1 HPFFRTRACDILLOPDNLACPKFVKPRNLINISQHGSDMVSFDPHAPNFGFRFFVLYHK 60
QY 215 LXHEGPFKKTKQEQTTTSCLLQNVSPGDIYIELVDVDTNTTKVMHYALKPVHSPWA 274
DB 61 LXHEGPFKKTKQEQTTTSCLLQNVSPGDIYIELVDVDTNTTKVMHYALKPVHSPWA 120
QY 275 GPRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAALPRERLRPR 334
DB 121 GPRAVAITVPLVWISAFATLFTVMCRKKQENIYSHLDEESSESTYTAALPRERLRPR 180

QY 335 PKVFLCYSSKGGQNMVWVQCFAIFLQDFCGCEVALDLWDFSLCREGQEWIWKIHES 394
DB 181 PKVFLCYSSKGGQNMVWVQCFAIFLQDFCGCEVALDLWDFSLCREGQEWIWKIHES 240
QY 395 QFIIVVCSKGMKVFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRQAKQSSAALSKEF 454
DB 241 QFIIVVCSKGMKVFVDKKNYKHGGGRSGKGEFLVAVSAIAEKLRQAKQSSAALSKEF 300
QY 455 IAVFYDSCGDDVPGIILDLSTKYRLMDNLPLQCSHLHSRDHGLQEPQHTROGSRNRYFR 514
DB 301 IAVFYDSCGDDVPGIILDLSTKYRLMDNLPLQCSHLHSRDHGLQEPQHTROGSRNRYFR 360
QY 515 SKGRSLYVAICNNHQFIDEEPWFKEQFVPFPPLRYREPVLKPDGSLVNDVMCKP 574
DB 361 SKGRSLYVAICNNHQFIDEEPWFKEQFVPFPPLRYREPVLKPDGSLVNDVMCKP 420
QY 575 GPESDFCLKVEAAVLGATGADSOHESQHGGLDODGEARPDALDGSAAALQPLHTTVKAGSP 634
DB 421 GPESDFCLKVEAAVLGATGADSOHESQHGGLDODGEARPDALDGSAAALQPLHTTVKAGSP 480
QY 635 SDMPRDSGIYDSSVPSSELSPLMEGLSTDOTETSSLTSSVSSSGLGEEPPALPSKLL 694
DB 481 SDMPRDSGIYDSSVPSSELSPLMEGLSTDOTETSSLTSSVSSSGLGEEPPALPSKLL 540
QY 695 SSGCKADLGRSYTDELHVAAPL 718
DB 541 SSGCKADLGRSYTDELHVAAPL 564

RESULT 8

Q7T2L7 PRELIMINARY; PRT; 741 AA.
ID Q7T2L7
AC Q7T2L7
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE FGF signalling antagonist SEF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22660508; PubMed=12766772; DOI=10.1038/ncb989;
RA Kawakami Y., Rodriguez-Leon J., Koth C.M., Buscher D., Itoh T.,
RA Raya A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
RA Schwarz M.-F., Asahara H., Izpisua Belmonte J.C.;
RT "MKP3 mediates the cellular response to FGF8 signalling in the
RT vertebrate limb";
RL Nat. Cell Biol. 5:513-519(2003).
DR EMBL; AY278204; AAP70001.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
SQ SEQUENCE 741 AA; 83553 MW; 64B8E88241AC60CF CRC64;

Query Match 74.3%; Score 2844; DB 2; Length 741;
Best Local Similarity 74.0%; Pred. No. 3.9e-207;
Matches 533; Conservative 75; Mismatches 94; Indels 18; Gaps 5;

QY 1 ADTCGWRKMAAARPLCVANEGVGPASRNSGLYNTTFKYDNCCTYLNVPVGHVIAQAONI 60
DB 38 ADACGR-----GLSSVTKSNGLLNITFKYDNCCTPYLNSVGKHVIGDVQNI 83
QY 61 TISQACHDQAVTILWSPGALGIEFLKGFVRVILELSEKSGQCQOLILKDPQLNSSPK 120
DB 84 TISQACHDQAVTILWSPGALGIEFLKGFVRVILELSEKSGQCQOLILKDPQLNSSPK 143
QY 121 RTGMESQPLNMKFTDYFKVVPFPIKNSNHYHFFRFTACDILLOPDNLACKPFWK 180
DB 144 RTGMESNPFANLKFTDYFKVVPFPIKNSNHYHFFRFTACDILLOPDNLACKPFWK 203

DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
KW Receptor.
SQ SEQUENCE 594 AA; 66780 MW; EABE6B655DC4EC3 CRC64;

Query Match 69.9%; Score 2675.5; DB 2; Length 594;
Best Local Similarity 84.8%; Pred. No. 1.8e-194;
Matches 507; Conservative 34; Mismatches 50; Indels 7; Gaps 4;

Qy 124 MESQFLNMKPTDYFKVVPFPFSGIKNESNYHPPFTRACDILLQPDNLACKPFWKPRN 183
Db 1 MESQFLNMKPTDYFKVVPFPFSGIKNESNYHPPFTRACDILLQPDNLACKPFWKPRN 60

Qy 184 LNIHQSGDMQVSDHAPNPFYFVLYKHLKHEGPFKTKQBOQTETTSCLLNQVS 243
Db 61 LNIHQSGDMHVSFDHAPNPFYFVLYKHLKHEGPFKTKQBOQTETTSCLLNQVS 120

Qy 244 PGDYIIELVDNTNTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 303
Db 121 PGDYIIELVDNNTTKAAQVTVKSVQSPWAGPIRAVAITVPLVVISAFATLFTVMCRKK 180

Qy 304 QQENIYSHLDESSSTYTAALPRRLRPKPVFLCYSSKQGNHNVVQCFAYFLQDF 363
Db 181 QQENIYSHLDESSSTYTAALPRDLRPQKPVFLCYSNKQGNHNVVQCFAYFLQDF 240

Qy 364 CGCEVALDLWDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRGS 423
Db 241 CGCEVALDLWDFSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGSRGE 300

Qy 424 KGELFLVAVSAIAELKRAQSSAALKRKFIAYFYDSCGDVPGILDSTKYRLMDNL 483
Db 301 AQGEFFLVAVAAIAELKRAQSSAALKRKFIAYFYDSCGDVPGILDSTKYRLMDHL 360

Qy 484 POLCSHLHSDHGLQEP--GQHTROGSRNRYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 542
Db 361 PELCAHLHS-----GQEVLGQHPGHSRRNRYFRSKGRSLYVAICNMHOFIDEEPDPWEKQ 417

Qy 543 FVPFHPPLRYREPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGPADSQH--E 600
Db 418 FIPQHPVPVRYREPVLKFDGLVNDVSKGPESDFCRKVEACVLGAAGPADSYLYE 477

Qy 601 SQHGLDQDGAAPALDGAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEG 660
Db 478 SQHGLDQDTEAQPSCDSAPALQPLLHVAVKAGSPSEMPRDSGIYDSSVPSSLSLPLMEG 537

Qy 661 LSTQDTETSSLTESVSSSGGEEPPALPSKLLSSGCKADLGCRSYTDELHVAAPL 718
Db 538 LSPDQIETSSLTESVSSSGGEEPPALPSKLLFASGVSR--EHGCHSHTDELQALAPL 594

RESULT 11
Q8R5J8 PRELIMINARY; PRT; 582 AA.
AC Q8R5J8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar expression to FGF protein (Fragment).
GN Name=musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21824237; PubMed=11802165; DOI=10.1038/ncb750;
RA Furthauer M., Lin W., Ang S.L., Thisse B., Thisse C.;
RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signalling."

Nat. Cell Biol. 4:170-174 (2002).
DR EMBL; AF424804; AAL79530.1; -
DR MGD; MGI:2159727; I117rd.
DR GO:0016020; C:membrane; IEA.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003676; F:nucleic acid binding; IEA.
DR GO:0004888; F:transmembrane receptor activity; IEA.
DR GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 1.
FT NON TER 1
SQ SEQUENCE 582 AA; 65263 MW; 56663B2981C4268E CRC64;

Query Match 68.3%; Score 2616.5; DB 2; Length 582;
Best Local Similarity 84.6%; Pred. No. 5.4e-130;
Matches 496; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

Qy 136 TDYFVKVVPFSPKSNESNYHPPFTRACDILLQPDNLACKPFWKPRNLSHQSGDMQV 195
Db 1 TDYFVKVVPFSPKSNESNYHPPFTRACDILLQPDNLACKPFWKPRNLSHQSGDMHV 60

Qy 196 SFDHAPNPFYFVLYKHLKHEGPFKTKQBOQTETTSCLLNQVS PGDYIIELVDNT 255
Db 61 SFDHAPNPFYFVLYKHLKHEGPFKTKQBOQTETTSCLLNQVS PGDYIIELVDNT 120

Qy 256 NTRKVMHYALPKVHSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 315
Db 121 NTRKAAQVTVKSVQSPWAGPIRAVAITVPLVVISAFATLFTVMCRKKQENIYSHLDEE 180

Qy 316 SSESSTYTAALPRRLRPKPVFLCYSSKQGNHNVVQCFAYFLQDFCGCEVALDLWED 375
Db 181 SPESSTYTAALPRDLRPQKPVFLCYSNKQGNHNVVQCFAYFLQDFCGCEVALDLWED 240

Qy 376 FSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGKGLFLVAVSA 435
Db 241 FSLCREGQREWIQIHESQFIIVVCSKGMKYFVDKKNYKHGGGRSGKGLFLVAVAA 300

Qy 436 IAEKLRQAKSSAALKRKFIAYFYDSCGDVPGILDSTKYRLMDNLQCLSHLSRDH 495
Db 301 IAEKLRQAKSSAALKRKFIAYFYDSCGDVPGILDSTKYRLMDHLPELCAHLHS--- 357

Qy 496 GLQEP--GQHTROGSRNRYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVFPHPPLRY 554
Db 358 GEQEVLGQHPGHSRRNRYFRSKGRSLYVAICNMHOFIDEEPDPWEKQFVFPHPPVRYQ 417

Qy 555 EPVLKFDGLVNDVMCKPGPESDFCLKVEAAVLGATGPADSQH--ESQHGGLDQDGEA 612
Db 418 EPVLKFDGLVNDVSKPGPESDFCRKVEACVLGAAGPADSYLYESQHVGLDQDTEA 477

Qy 613 RPAIDGSAALQPLLHTVTKAGSPDMPRDSGIYDSSVPSSLSLPLMEGLSTDQETSSLT 672
Db 478 QPSCDSAPALQPLLHVAVKAGSPSEMPRDSGIYDSSVPSSLSLPLMEGLSPDQIETSSLT 537

Qy 673 ESVSSSGGEEPPALPSKLLSSGCKADLGCRSYTDELHVAAPL 718
Db 538 ESVSSSGGEEPPALPSKLLASGVSR--EHGCHSHTDELQALAPL 582

RESULT 12
Q8QHJ9 PRELIMINARY; PRT; 745 AA.
AC Q8QHJ9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sef.
GN Name=ill7rd; Synonyms=sf; (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;


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Db      100 LQTDASILYLEGAELSVLQNTNERLCVR--FEFLSKLRHHRRWRFTFSHFV-VDPDOE 156
Qy      138 YFVKV--VPPPSIKNESNYHPFFRTRACDLLQPDNLACK---PFWKPRNL----- 184
Db      157 YEVTVHLPKPPIPDGDPNHOSKNFLVPDCEHARMKVTTPCMSGSLWDP-NITVETLEAH 215
Qy      185 -----NISQHGSDMQVSFDHAPHNFGFRFPYLVKLEHGPFRKTKCKQEQTTETT 235
Db      216 QLRVSFTLWNESTHYQILLTSFPHMENHSCFEHMH-HIPAPRPEEFQORSNVILTLENLK 274
Qy      236 SCLLQNVSPGDYIITELVDDT---NTTRKVMHYALKPVHSPWAGPIRAVAITVPLVWISAF 292
Db      275 GCCRHQVQIQPFSSCLNCLRHSAVSCPEMDTPPEIPDYMLWVYWFITGISILLVG 334
Qy      293 ATLETVMCRKKQQENIYSHLDEESSESTYTAALPRERLRPRP-----KVFLCYSSKDGQN 348
Db      335 SVILLIVMTWRLAGPGS--EKYSDDTKYTDGLPVADLIPPLKPRKVMIIYSA-DHPL 390
Qy      349 HMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREQREWV---IQTHESQFIIVVCSKG 404
Db      391 YVDVVLKPAQFLLTACGTEVALDLLEEQATSEAGVMTWVGRQKQEMVESNKIIVLCERG 450
Qy      405 MKYFVDKKNYKHGGG-----RSGSGELFLVAVSAIAEKLROAKQSSAALSXFIA 456
Db      451 TR----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAMNMLPDFKR-----PACFGTYVV 501
Qy      457 VYF-DYSCGEGVPGILDSTKYRLMDNLPQLCSHLHSRDHGLQBPQOHTROG--SRNRYF 513
Db      502 CYFEVSCDGDVDPDLFGAAPRYPLMDRFEEV--YFRIQDLEMFPQGRMHRVGLSGDNYL 559
Qy      514 RSKSGRSIYVAICNMHQFIDEEDPWE-----KQFVPPHPPPLYRBPVLEKFDGSL 565
Db      560 RSPGGRQLRAALDRFRDQVHCDFWFCENLYSADDDQDAPSLDEEV-FEBPLLP-GTGI 617
Qy      566 VLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHE-----SQHGG 605
Db      618 VKRAPLVRE-PCSQACLAIDPLVGEEGGAIVAKLEPHLQPRGQAPQPLHTLVLAEEGA 676
Qy      606 LDQDGEARPALDGA---ALQ-----PLLHTVKGSPDMPRDSGIYDSSVPSSLSLP 656
Db      677 LVAAVEPGPLADGAAVRLALAGEGEACPLLGSFGAG-----RNSVLF---LPVDPEDSP 727
Qy      657 LMEGLSTDQETSTTSVSSSSGLGEEPPALPSKLLSSGCKADLGC 705
Db      728 L--GSSTPMASPDLLPEDVR-----EHLEGLMLSLFEQSLSCQAQGGC 768
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Job time : 117.24 secs